class

Human HLA
Taste mod
Human HGP
CD66 pept
CD66 pept
CD66 pept
Human CD6
Iuman HGP
Uman HGP
Uman HGP

Adm12345
Ado38565
Ado38565
Aar67090
Abu191918
Aab88018
Aab88018
Aab86059
Abu11935

G protein DNA clone Insulin/i

IGF-1R re

us-09-936-956-1.rag

score:

Perfect

е 6

Run

Sequence:

Scoring table:

Searched:

Minimum DB E Maximum DB E

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This invention relates to a novel composition which comprises at least one protein (or fragment of) encoded by an open reading frame (ORF) of a Neisseria sp. (ORF2086), where the ORF encoding a crossreactive immunogenic antigen provides immunogenicity against infection by Neisseria meningitidis serogroup B in a subject. The composition of the invention may have antibacterial or antiinflammatory activity through the induction of the immune response. The invention may be useful for the treatment of bacterial meningitis in a mammal. One or more polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Composition comprising crossreactive immunogenic antigen encoded by open reading frame 2086 of Neisseria sp., that provides immunogenicity against meningitis, or its immunogenic portion or biological equivalent.
                                                                                                                                                                                                                                                                                                                      ORF2086; Neisseria meningitidis serogroup B infection; antibacterial; antinflammatory; immune response; bacterial meningitis; Streptococcus pneumoniae infection; non-pathogenic; immunogenic composition; 2086 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Farley J, Bernfield LA,
                                                                                                                                                                                                                                                                                                      Neisseria meningitidis ORF2086 protein SeqID248.
                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 60; SEQ ID NO 248; 480pp; English
                 ADM12345
ADO38565
                                  ADP80010
AAR67090
ABU11918
AAB88073
AAB88018
AAB88059
AAB88056
ABP67248
ABU11935
                                                                                                                            ABU11944
ABU11956
                                                                                                                                              ABP83373
                                                                                                                                                       ABM74254
                                                                                                                                                                AAU89150
                                                                                                                                                                         ADA03975
                                                                                                                                                                                                                                                  ADE44814 standard; protein; 260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             11-OCT-2001; 2001US-0328101P.
30-AUG-2002; 2002US-0406934P.
                                                                                                                                                                                                                                                                                                                                                                                                                            11-OCT-2002; 2002WO-US032369
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C B B B B C D A A A A A D D D D D D D D D
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                                                                                                                                                                                                                                                                                    (first entry)
Fletcher
                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis.
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N-PSDB; ADE44813.
WO2003063766-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zlotnick GW,
                                                                                                                                                                                                                                                                                    29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metcalf BJ
ADE44814;
                                                                                                                                                                                                                               RESULT 1
                                                                                                                                                                                                                                         ADE44814
rsaA S-ly
Caulobact
Caulobact
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HLA-A24 r
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HLA-A24
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                                                                       (without alignments)
184.386 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                              February 24, 2005, 15:03:10 ; Search time 117.463 Seconds
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                                                                                                                   Aay44757
Aae34374
Add21187
Add72935
Aay00829
Aay00839
Aay00839
Aay00833
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Adf83690 1
Adg38740 1
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Aaw37490
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        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                2105692 seqs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                            using sw model
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ADP80011
ADD23187
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AAY46550
AAY00829
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AAY00833
AAY00835
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AAY00828
AAY00834
AAY00832
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                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
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geneseqn1990s:*
geneseqn2000s:*
geneseqn2001s:*
geneseqn2001s:*
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seq length: 200000000
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274
1026
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                                            OM protein - protein search,
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Match
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Database

Zagursky RJ;

Result

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition comprising crossreactive immunogenic antigen encoded by open reading frame 2086 of Neisseria sp., that provides immunogenicity against meningitis, or its immunogenic portion or biological equivalent.
or nucleic acids encoding such polypeptides are useful in a composition or as a part of the treatment regimen for the prevention of amelioration of Streptococcus pneumoniae infection. The composition of the invention is non-pathogenic and substantially free from any infectious impurities. The immunogenic compositions can be compounded with fewer components to elicit protection compazable to previously used agents. The present sequence is the amino acid sequence of a Neisseria meningitidis strainspecific mature 2086 protein with a native leader sequence which can be used to create the composition of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORF2086; Neisseria meningitidis serogroup B infection; antibacterial; antiinflammatory; immune response; bacterial meningitis; Streptococcus pneumoniae infection; non-pathogenic; immunogenic composition; 2086 protein.
                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                  25.5%; Score 25; DB 7; Length 260; 25.0%; Pred. No. 1.5e+03; ive 0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis ORF2086 protein SeqID252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 60; SEQ ID NO 252; 480pp; English.
                                                                                                                                                                                                                                                                                                                                     56
                                                                                                                                                                                                                                                                                                                                                                         71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.
                                                                                                                                                                                                                                                                                                                                   33 NGTFXXXXXXXXXXGDXXXXG
                                                                                                                                                                                                                                                                                                                                                                           NGTLTLSAQGAEKTYGNGDSLNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADE44818 standard; protein; 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-OCT-2001; 2001US-0328101P. 30-AUG-2002; 2002US-0406934P.
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                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis.
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                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                              Sequence 260 AA;
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Metcalf BJ;
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                                                                                                                                                                                                                                                                                                                                                                           48
                                                                                                                                                                                                                                                  Query Match
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ID ADE
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This invention relates to a novel composition which comprises at least one protein (or fragment of) encoded by an open reading frame (ORF) of a Neisseria sp. (ORF2086), where the ORF encoding a crossreactive immunogenic antigen provides immunogenicity against infection by Neisseria meningitidis serogroup B in a subject. The composition of the immune response. The invention may bave antibacterial or antiinflammatory activity through the induction of the immune response. The invention may be useful for the treatment of bacterial meningitis in a mammal. One or more polypeptides or nucleic acids encoding such polypeptides are useful in a composition of ras a part of the treatment regimen for the prevention of amelioration of Streptococcus pneumoniae infection. The composition of the invention is non-pathogenic and substantially free from any infectious impurities. The immunogenic compositions can be compounded with fewer components to elicit protection comparable to previously used agents. The present sequence is the amino acid sequence of a Neisseria meningitidis strain-
                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition comprising crossreactive immunogenic antigen encoded by open reading frame 2086 of Neisseria sp., that provides immunogenicity against meningitis, or its immunogenic portion or biological equivalent.
The immunogenic compositions can be compounded with fewer components to elicit profection comparable to previously used agents. The present sequence is the amino acid sequence of a Noisseria meningitidis strainspecific mature 2086 protein which can be used to create the composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibacterial;
                                                                                                                                                                                                             Gaps
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0
                                                                                                                                                                     Length 260;
                                                                                                                                                                                                           18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORF2086; Neisseria meningitidis serogroup B infection; ar antiinflammatory; immune response; bacterial meningitis; Streptococcus pneumoniae infection; non-pathogenic; immunogenic composition; 2086 protein; P4 leader.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis ORF2086 protein SeqID250.
                                                                                                                                                                   1 25.5%; Score 25; DB 7; 1 Similarity 25.0%; Pred. No. 1.5e+03; 6; Conservative 0; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 60; SEQ ID NO 250; 480pp; English
                                                                                                                                                                                                                                                      33 NGTFXXXXXXXXXXXG 56
                                                                                                                                                                                                                                                                                           48 NĠTLTLSAQGAEKTYGNĠĎSLNTĠ 71
                                                                                                                                                                                                                                                                                                                                                                                                      ADE44816 standard; protein; 261 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis.
Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-663416/62.
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Best Local Similarity
                                                                                     the invention.
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                                                                                                                            Sequence 260 AA
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Gaps

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18; Indels

Score 25; DB 8; L Pred. No. 1.6e+03; 0; Mismatches 18;

25.5%;

Conservative

33 NGTFXXXXXXXXXXXGDXXXXG 56

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85

NGTLTLSAQGAEKTYGNGDSLNTG

AAR48993 standard; protein; 1026 AA

RESULT 5 AAR48993 (first entry)

rsaA S-lyaer protein.

(revised)

16-OCT-2003 14-SEP-1994

AAR48993;

Length 274;

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The present invention relates to composition (1) comprising at least two multiple variants of meningococcal protein NMB1870 (ADP70202-ADP70246, ADP70280-ADP70280-ADP70286, ADP70280-ADP70280, ADP70280-ADP70280, ADP70280-ADP70280, ADP70280-ADP70280, ADP70280-ADP70280, ADP70280-ADP70280, attribute against each of antipody response which is bactericidal against each of serogroup B Neisseria meningitidis strains MC59, 961-5945 and M1239, and meningitidis strains in at least 2 of hypervirulent lineages ET-37, ET-5, cluster A4, lineage 3, subgroup I, subgroup II, and subgroup IV-1. In NMB1870 is a lipoprotein. In (1) at least one of the proteins does not include the amino acid sequence ADP70271 or ADP70272 within 10 amino acid sequences ADP70271 or ADP70272 within 10 amino acid sequences ADP70273 within 10 amino acid sequences ADP70273 within 10 amino acid sequences ADP70273 within 10 amino acid sequence accordance and accordance and/or mucosal immunity and thereby prevents/treat meningitis and and and accordance accordance accordance accordance a
                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibacterial; Antiinflammatory; Vaccine; meningococcal protein; NMB1870; antigen; bactericide; meningitis; bacteraemia; Neisserial infection;
specific mature 2086 protein with a P4 leader sequence (derived from the Haemophilus influenzae P4 protein) which can be used to create the composition of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Composition for producing medicament for preventing Neisserial infection in mammal, comprising multiple variant of meningococcal protein NMB1870,
                                                                                                                                                                                                                  Gaps
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                                                                                                                                                     25.5%; Score 25; DB 7; Length 261; 25.0%; Pred. No. 1.5e+03; ive 0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis NMB1870 protein, SEQ ID 128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis; strain ISS1113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; SEQ ID NO 128; 77pp; English.
                                                                                                                                                                                                                                                              33 NGTFXXXXXXXXXXXX 56
                                                                                                                                                                                                                                                                                                                49 NGTLTLSAQGAEKTYGNGDSLNTG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP70329 standard; protein; 274 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-NOV-2002; 2002GB-00027346
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                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Comanducci M, Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-468293/44.
                                                                                                                                                                                 Best Local Similarity
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                                                                                                      Sequence 261 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lipoprotein.
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                                                                                                                                                           Query Match
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C. crescentus; rsaA; paracrystalline; S-layer; protein; heterologous; cellulase; xylase; metallothionein; restriction site; reading frame; fusion protein; bioreactor; toxic metal; sewage; waste water; wood pulp suspension; cell surface; vaccine; fish.

Caulobacter vibrioides

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This sequence is encoded by the C. crescentus rsaA gene and represents the paracrystalline S-layer protein. The rsaA gene was used in the production of the heterologous protein of the invention. The heterologous protein is produced by cloning a polypeptide coding sequence, eg. cellulase, xylase or a metallothionein, into a restriction site within the rasA gene which preserves the rsaA reading frame and expressing the twiston sequence in Caulobacter. This S- layer protein bacterial system can be used in bioreactors, eg. to bind toxic metals in sewage waste water etc. or for the treatment of wood pulp suspensions. The system can be used to produce heterologous proteins at the cell surface for use in vaccines, partic. fish vaccines. The S-layer protein is synthesised in large quantities and has a general repetitive sequence, permitting the large amounts of heterologous protein as a fusion product and presentation at the cell surface. (Updated on 16-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267 NDTFVAGEVAGAATLTVGDTLSGG 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 17; Fig 6; 27pp; English.
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Matches 6; Conserv
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8
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Sequence 274 AA;

Prodn. of heterologous polypeptides in bacteria, partic. Caulobacter - by expression of a fusion prod. of the polypeptide sequence and a bacterial S-layer protein gene.

(UYBR-) UNIV BRITISH COLUMBIA.

WPI; 1994-066249/09. Smit J, Bingle WH;

N-PSDB; AAQ57972

93CA-02090549. 92US-00895367.

26-FEB-1993; 09-JUN-1992;

10-DEC-1993

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Caulobacter crescentus S-layer rsaA protein.
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                                                                                                                                                                                            WPI; 1997-470880/43.
N-PSDB; AAV01866.
                                                                                                                                                                         Smit J, Bingle WH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1026 AA;
                                      wood pulping.
                                                                          WO9734000-A1.
                                                                                                                10-MAR-1997;
                                                                                                                                   12-MAR-1996;
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04-MAY-2000
                                                                                             18-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY44757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY44757
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                                                                                                                                                                                                                                                                                                                                                                                                                          The Caulobacter crescentus CB15 paracrystalline S-layer protein (AAR17717) is encoded by the reaA gene (AAR17717). It can be used as a fusion partner with polypeptides of interest, allowing presentation of the polypeptide on the surface of the Caulobacter cells. The bacterium is cultured as a biofilm in a bioreactor or may be used to present an artigenic epitope (see ARR94016 and AAR94018) to the environment e.g. for use as a vaccine. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                          Expression and presentation of polypeptide heterologous to Caulobacter S-layer protein to bacterium's environment - by cloning in-frame into Caulobacter reak gene, and expressing as fusion prod. with S-layer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                 860. .905
/note= "glycine-aspartic acid repeat region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.5%; Score 25; DB 2; Length 1026; 25.0%; Pred. No. 6.2e+03; Live 0; Mismatches 18; Indels
                                                                                                                                S-layer; rsaA gene; surface protein; biofilm; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 NDTFVAGEVAGAATLTVGDTLSGG 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 NGTFXXXXXXXXXXGDXXXXG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW37490 standard; protein; 1026 AA.
                                    AAR94014 standard; protein; 1026 AA.
                                                                                                                                                    Caulobacter vibrioides; strain CB15.
                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Fig 6a-c; 22pp; English.
                                                                                                                                                                                                                                                                                         (UYBR-) UNIV BRITISH COLUMBIA
                                                                                                                                                                                                                                                    94US-00194290.
                                                                                                                                                                                                                                                                      92US-00895367
                                                                                                              Caulobacter S-layer protein.
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Best Local Similarity 25.00,
Conservative
Conservative
                                                                         (revised)
(revised)
(first entry)
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(first entry)
                                                                                                                                                                                                                                                                                                                              WPI; 1996-171046/17.
N-PSDB; AAT17717.
                                                                                                                                                                                                                                                                                                            Bingle WH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1026 AA;
                                                                                                                                                                                                                                                    09-FEB-1994;
                                                                                                                                                                                                                                                                      09-JUN-1992;
                                                                                            21-MAY-1996
                                                                                                                                                                                                              US5500353-A.
                                                                                                                                                                                                                                 19-MAR-1996.
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20-APR-1998
                                                                         16-OCT-2003
25-MAR-2003
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                                                       AAR94014;
                                                                                                                                                                                                                                                                                                            Smit J,
                                                                                                                                                                                                                                                                                                                                                                                          protein.
                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW37490
ID AAW:
XX AC AAW:
XX DT 17-4
DT 20-;
                 RESULT 6
                           AAR9401
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The present sequence represents a Caulobacter S-layer protein used in an example of the present invention. A new DNA construct has been developed which contains at least one restriction site for insertion of DNA upstream of DNA encoding a C-terminal region of at least the last 82 amino acids (aa) of Caulobacter S-layer protein. Caulobacter containing the DNA constructs above additionally containing a sequence encoding a heterologous polypeptide, are particularly useful in live vaccines (where the DNA constructs above additionally containing a sequence encoding a heterologous polypeptide is an antigen). They can also be used for production of e.g. ligands, enzymes or other proteins, e.g. production of e.g. ligands, enzymes or other proteins, e.g. metallothionalist or remove heavy metals from water or sewage, or xylanase or callulase for use in wood pulping All known Caulobacter strains are harmless, and stable in outdoor environments, including water (so suitable for waccinating fish) or soil. They are well suited for growing in biofilm reactors and produce S-layer proteins, which is an ideal system for presentation of antigens, at high level. (Updated on 17-OCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA containing sequence for C-terminal region of Caulobacter S-layer protein - expressed as fusion proteins containing antigenic peptides in Caulobacter, useful as live vaccines.
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S-layer; rsaA gene; Caulobacter; vaccine; antigenic; ligand; enzyme; metallothionein; heavy metal; water; sewage; xylanase; cellulase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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25.0%; Pred. No. 6.2e+03;
iive 0; Mismatches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nomellini JF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Fig 6; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYBR-) UNIV BRITISH COLUMBIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-00614377.
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Best Local Similarity 25.0%,
Conservative
G, Conservative
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                                                                                                                                                                       Caulobacter vibrioides.
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Smit J;

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The present invention relates to Caulobacter deficient in a protease native to Caulobacter that cleaves hybrid Caulobacter S-layer protein monomers. The Caulobacter is useful as a host cell for expression of a hybrid Caulobacter S-layer protein monomer or for the expression of heterologous peptides. The Caulobacter is also useful as an expression system for producing random libraries of peptides or gene fragments for display and panning purposes. This system is useful for the expression of unknown or uncharacterised peptides. The present sequence is Caulobacter crescentus RsaA protein. (Updated on 23-OCT-2001 to standardise OS field)
                                                                                                                                                                                                                                                                                       New Caulobacter deficient in a protease native to Caulobacter that cleaves hybrid Caulobacter S-layer protein monomers, useful as a host cell for expressing a hybrid S-layer protein monomer, or for expressing heterologous peptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epitope; HLA-A1; HLA-A2; HLA-A3; HLA-A24; HLA-B7; HLA-B44; tumour associated antigen peptide; cytostatic; vaccine; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 1026;
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25.0%; Pred. No. 6.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human HLA-A24 epitope vaccine peptide SeqID266.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 NDTFVAGEVAGAATLTVGDTLSGG 290
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                                                                                                                                                                                                    Smit J, Nomellini JF, Bingle WH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP80011 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 6; Page 8; 49pp; English
                                                                                                                                                      (UYBR-) UNIV BRITISH COLUMBIA
                                                                                                           22-MAY-2001; 2001CA-02347657.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-DEC-2003; 2003WO-US038949
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                                                                22-MAY-2002; 2002WO-CA000722
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Best Local Similarity 25.03
Matches 6; Conservative
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                                                                                                                                                                                                                                                 WPI; 2003-148470/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1026 AA;
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                28-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The patent discloses a method for cleaving a recombinant fusion protein which is produced by Caulobacter and consists of Caulobacter surface layer (S-layer) protein (containing the C-terminal secretion signal) and a target protein heterologous to Caulobacter. The cleavage of target protein heterologous to Caulobacter. The cleavage of target protein heterologous to canditions so that cleavage occurs at aspartate proline dipeptide site without solubilishing the protein. The cleavage is accomplished while the fusion protein is no macoluble aggregate form which facilitates protein in an insoluble aggregate form which facilitates protein in the protein. The method is useful for producing pure protein including recombinant human and animal therapeutic antibiotic and vaccine peptides, enzymes, protein polymers, and antibacterial curymes for foodstuffs. The present sequence is a S-layer protein from C crescentus. The S-layer secretion signal, corresponding to the C-terminal portion of the protein from amino acid 690 onwards, is fused with a target sequence for construction of a recombinant fusion construct which is a spressed in Caulobacter. (Updated on 12-SEP-2003 to standardise OS
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                                                    /note= "Asp-Pro dipeptide present in S-layer secretion signal sequence. It is a site where a fusion protein comprising a target protein and the secretion signal is cleaved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cleavage of Caulobacter produced recombinant fusion proteins useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caulobacter crescentus RsaA protein.
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                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                    98CA-02237704.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     producing vaccine peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-182434/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAZ50079
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                                                                                                                                                                                 WO200004170-A1
                                             Cleavage-site
                                                                                                                                                                                                                                                                       14-JUL-1999;
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14-MAY-2003
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Query Match

Matches

AAE34374

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Gaps

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18; Indels

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                                         This invention relates to a novel isolated peptide which comprises at least 1, 2, 3, 4, 5, 6 or 7 epitopes or analogues of the epitopes given in the specification. The peptide comprises HLA-A1, A2, A3, A24, B7 or B44 tumour associated antigen peptide. The invention may be useful for the production of compounds with a cytostatic activity or for the production of a vaccine. The peptide is useful in preparing a composition diagnosing or treating tumour associated antigen-related disease. The present sequence is that of an epitope peptide for use in the peptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method of screening for and/or diagnosing breast cancer in a subject, and/or monitoring the effectiveness of breast cancer therapy. The method comprises detecting and/or quantifying in a biological sample obtained from the subject a breast cancer membrane protein (BCMP) polypeptide and a nucleic acid molecule. Also described: (1) an antibody, its functionally-active fragment, derivative or analogue, that specifically binds to one or more of the BCMP polypeptide; (2) a diagnostic kit comprising a capture of the BCMP polypeptide, reagents and instructions for use; (3) a method for screening for anti-breast cancer agents that interact with the BCMP polypeptide, comprising contacting the polypeptide agent interact with the polypeptide; (4) a method for screening for anti-breast cancer agents that modulate the expression or activity of an BCMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening, diagnosing and/or treating breast cancer by detecting a change in expression or activity of a breast cancer membrane protein (BCMP)
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             breast cancer; screening; diagnosis; breast cancer therapy; breast cancer membrane protein; BCMP; cytostatic; vaccine; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Breast cancer membrane protein (BCMP) peptide SEQ ID NO:617.
                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                               Length 8;
                                                                                                                                                                                                                                           23.5%; Score 23; DB 8; Le
100.0%; Pred. No. 1.8e+06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide or encoding nucleic acid molecule.
               Claim 1; SEQ ID NO 266; 244pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; SEQ ID NO 617; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Terrett JA;
                                                                                                                                                                                                                                                                                                                                                                                                                               ADD23187 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-APR-2003; 2003WO-GB001559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-APR-2002; 2002GB-00008331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                           Local Similarity 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hudson LJ, Stamps AC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-845381/78.
                                                                                                                                                                                                                                                                                                              NGTF 36
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                                                                                                                                                                                                                                                                                                                                   NGTF
                                                                                                                                                                                                              Sequence 8 AA;
                                                                                                                                                                                the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADD23187;
                                                                                                                                                                                                                                                                                                                33
                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                ADD23187
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                 comparing the expression or activity of the polypeptide or nucleic acid molecule, in the presence and absence of a candidate agent or in the presence of a control agent, and determining whether the candidate agent causes the expression or activity of the polypeptide or nucleic acid molecule to change; and (5) an agent identified by the method of (3) or 4), which interacts with the polypeptide or causes the expression or activity of the polypeptide, or the expression of the nucleic acid molecule to change. BCMPs have cytostatic activities, and can be used in vaccines. The BCMP polypeptide, nucleic acid molecule, and can be used in their derivatives, are useful in the manufacture of a medicament for the treatment of breast cancer, where the composition is a vaccine. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptides and encoding nucleic acids that are useful epitopes of target-associated antigens, useful for diagnosing and/or treating viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
polypeptide or the nucleic acid molecule cited above, comprising
                                                                                                                                                                                                                                                                                present sequence represents a BCMP peptide which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                             23.5%; Score 23; DB 7; Length 9; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                     exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 194; 357pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADM72935 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human CEA epitope SEQ ID NO:194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infections, cancers and tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-SEP-2003; 2003WO-US027706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diamond DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MANN-) MANNKIND CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-315564/29.
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 NGTF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 NGTF 7
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                                                                                                                                                                                                                                                                                                                                                    Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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Length 10;

1.5e+02; DB 2;

Query Match

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100.0%; Prec. ...ive 0; Mismatches
Score 23;
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97JP-00203917.
98JP-00014736.
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23.5%;
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Tanaka F, Kato I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TAKI ) TAKARA SHUZO CO LTD.
                                                                                                                                                                                                                                                                              19-MAY-1999 (first entry)
                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
Query Match
Best Local Similarity
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                                                                     33 NGTF 36
                                                                                                   NGTF 10
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15-JUL-1997;
12-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                         AAY00829;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancers
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Matches
                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                 RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY45390 to AAY48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A3.2 or A24.1 or HLA-B or C) and induce a cytocoxic T cell response against the antigen from which the peptide is derived. Cytocoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in antigen in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to the peptide e.g. to produce CTLB ex vivo for infusion back into a patient. The polynucleotides encoding the immunosenic peptides are also useful therapeutically and for immunisation as above
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                                                                                                                                                                                                                                                                                                                                                                           Immunogenic peptide having a human leukocyte antigen binding motif #1161.
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                                                                                                                                                                                                                                                                                                                                                                                                          Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                           Gaps
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                                                                                       0; Indels
                                                    23.5%; Score 23; DB 8; Length 9; 100.0%; Pred. No. 1.8e+06;
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                                                                100.0%; Pred. ....
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                                                                                                                                                                                                                                                            AAY46550 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sette A, Kubo RT, Sidney J,
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                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                     Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccine; immunisation
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                                                                                                                            33 NGTF 36
                                                                                                                                                     NGTF
                   Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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Sequence 10 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIA-A24; antigenic peptide; cytotoxic T-lymphocyte; CTL; HLA-A24 complex;
cancer; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytotoxic T-lymphocytes recognising cells expressing HLA-A24/antigenic peptide complex - and inducing agents for them consisting of such antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yasumoto M, Iwasaki T, Ideno M, Akiyoshi T;
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Indels
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                                                                                                                                                                                                                                           AAY00829 standard; peptide; 10 AA.
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Nukaya I, Yac.
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97JP-00203917.
98JP-00014736.
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 (TAKI ) TAKARA SHUZO CO LTD.
                     Takesako K, Nukaya I, Yasu
Fujie T, Tanaka F, Kato I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TAKI ) TAKARA SHUZO CO LTD.
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                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-132220/11
                                                    WPI; 1999-132220/11
                                                                                                                                                                                                                                        Local Similarity
wes 4; Conserv
                                                                                                                                                                                                                                                                          33 NGTF 36
                                                                                                                                                                                                                                                                                              NGTF 10
                                                                                                                                                                                                             Sequence 10 AA;
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15-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                        cancers
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Matches
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                                                                                                                                                                                                                                                                                                               This sequence represents an HLA-A24 antigenic peptide sequence used in the cytotoxic T-lymphocytes (CTL) of the invention. The CTL recognise cells expressing on their surface a complex of an HLA-A24 molecule with an antigenic peptide. The antigenic peptide is an HLA-A24 restrained antigenic peptide. The CTLs can be used in the treatment and diagnosis of
                                                                                                                                                                                                                                                   Cytotoxic T-lymphocytes recognising cells expressing HLA-A24/antigenic peptide complex - and inducing agents for them consisting of such antigen
                  HLA-A24; antigenic peptide; cytotoxic T-lymphocyte; CTL; HLA-A24 complex;
cancer; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLA-A24, antigenic peptide; cytotoxic T-lymphocyte; CTL; HLA-A24 complex;
cancer; therapy; diagnosis.
                                                                                                                                                                                                  Akiyoshi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                              23.5%; Score 23; DB 2; Length 10;
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                                                                                                                                                                                                  Iwasaki T,
                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. ...
                                                                                                                                                                                                  Yasumoto M,
                                                                                                                                                                                                                                                                                              Example 9; Page 76; 88pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY00833 standard; peptide; 10 AA
 HLA-A24 antigenic peptide CE-203
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97JP-00203917.
98JP-00014736.
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98JP-00014736.
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Fujie I, Tanaka F, Kato I;
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                                                                                                                                                                            (TAKI ) TAKARA SHUZO CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                WPI; 1999-132220/11.
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                         presenting cells.
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15-JUL-1997;
12-JAN-1998;
                                                                      WO9903972-A1
                                                                                                                13-JUL-1998;
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12-JAN-1998;
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Cytotoxic T-lymphocytes recognising cells expressing HLA-A24/antigenic peptide complex - and inducing agents for them consisting of such antigen -presenting cells.
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cancer; therapy; diagnosis.
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 Akiyoshi
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 Ideno M,
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1.5e+02;
Iwasaki T,
                                                                                                                                                                                                                                                                                                                                                   23.5%; Score 23; DB
100.0%; Pred. No. 1.5
:ive 0; Mismatches
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Yasumoto M,
                                                                                                                                                           Example 9; Page 77; 88pp; Japanese.
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Cytotoxic T-lymphocytes recognising cells expressing HLA-A24/antigenic peptide complex - and inducing agents for them consisting of such antigen -presenting cells.
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                                                                                                     HLA-A24; antigenic peptide; cytotoxic T-lymphocyte; CTL; HLA-A24 complex; cancer; therapy; diagnosis.
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cancer; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                         Iwasaki T, Ideno M, Akiyoshi T;
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100.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 0;
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                                                                             HLA-A24 antigenic peptide CE-204.
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97JP-00203917.
98JP-00014736.
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Fujie T, Tanaka F, Kato I;
                                              19-MAY-1999 (first entry)
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Best Local Similarity 100.
Matches 4; Conservative
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12-JAN-1998;
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                AAY00831;
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cancer; therapy; diagnosis.
antigenic peptide. The CTLs can be used in the treatment and diagnosis
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                                                                           Length 10;
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                                                                          Score 23; DB 2; Le
Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                                                                              HLA-A24 antigenic peptide, CEA peptide CE-2.
                                                                                                        Mismatches
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AAY00831
ID AAY00831 standard; peptide; 10 AA.
                                                              23.5%; Scc_
100.0%; Pred
0; N
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97JP-00203917.
98JP-00014736.
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Fujie T, Tanaka F, Kato I;
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                                                           Query Match
Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                    7 NGTF 10
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This sequence represents an HLA-A24 antigenic peptide sequence used in the cytotoxic T-lymphocytes (CTL) of the invention. The CTL recognise cells expressing on their surface a complex of an HLA-A24 molecule with an antigenic peptide. The antigenic peptide is an HLA-A24 restrained antigenic peptide. The CTLs can be used in the treatment and diagnosis of cancers
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cancer; therapy; diagnosis.
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                                                                                                                                  DB 2; Lens.
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                                                                                                                                            23.5%; Score 23; DB 100.0%; Pred. No. 1.5 ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                            AAY00832 standard; peptide; 10 AA.
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Fujie T, Tanaka F, Kato I;
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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12-JAN-1998;
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Matches
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AAY00832
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                                                                                                                                                                      Cytotoxic T-lymphocytes recognising cells expressing HLA-A24/antigenic peptide complex - and inducing agents for them consisting of such antigen -presenting cells.
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cancer; therapy; diagnosis.
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naka F, Kato I;
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          97JP-00203900.
97JP-00203917.
98JP-00014736.
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98JP-00014736.
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Fujie I, Tanaka F, Kato I;
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                                                                   (TAKI ) TAKARA SHUZO CO LTD
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                                                                                   Takesako K, Nuκαχ...
Tanaka F,
                                                                                                                                            WPI; 1999-132220/11
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          15-JUL-1997;
15-JUL-1997;
12-JAN-1998;
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(first entry)

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Non-human transgenic mammals expressing HLA-A24 with cytotoxic T cells induced by HLA-A24-restricted antigenic stimulation, useful in screening preventives or remedies for tumor or viral infections.
                                                                                                                                                                                                                                                                                               non-human transgenic mammal; HLA-A24; cytotoxic T cell; CTL; tumour; viral infection; antigen; chimeric; cytostatic; virucide; human.
                                                                                                                                                                                                                                   HLA-A24 related human peptide, SEQ ID No 20.
                                                        ADF83690 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-DEC-2001; 2001WO-JP010885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-DEC-2000; 2000JP-00378556.
06-SEP-2001; 2001JP-00269746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-067332/06.
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                           26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUN-2002
                                                                                                                   ADF83690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gotoh M;
RESULT 24
                                  4DF8369(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to novel T-cell binding ligand (TCBL)

peptides (e.g. peptide G' (modified human MHC class II beta chain peptide

C peptide J (human beta-2-microglobulin peptide) and HIV-1 peptides) and

TCBL peptide Constructs for treating immunological disorders. The peptides

C patient. The method comprises administering the peptide construct to the

patient. The method comprises administering the peptide construct to the

patient preferably in combination with an immune response in a human

peptide constructs in the form of conjugated peptides are useful for

c peptide constructs in the form of conjugated peptides are useful for

c liciting a cellular immunodeficiency virus (HIV). The TCBL peptides

are useful for treating a patient suffering from an immunological

c are useful for treating a patient wifering from an immunological

c are useful for treating a patient suffering from an immunological

c are useful for treating a patient suffering from an immunological

c are useful for treating a patient of suffering from an immunological

c ansorder such as harpes simplex virus (HSV) infection, malaria,

t tuberculosis, cancers, acquired immunodeficiency syndrome (AIDS),

c allergies, autoimmune myocarditis, diabetes and lupus) by

c allergies, autoimmune myocarditis, diabetes and lupus) by

c administering a peptide construct comprising a TCBL peptide bonded to an

antigent peptide associated with the disorder. Unlike prior art peptide

conjugates, a modified version of peptide G has long range stabilisation

c and also enhances the immune response. AAU82019-AAU82114 represent T-cell

specific binding ligand peptides, peptide constructs or peptides in their construction
                                                                                                                                                                                                                                                                                                                    T-cell binding ligand; TCBL; peptide G'; human MHC class II beta chain; peptide J; human beta-2-microglobulin; HIV-1; TCBL peptide construct; immunological disorder; immune response; human immunodeficiency virus; herpes simplex virus infection; HSV; malaria; tuberculosis; cancer; CEA; acquired immunodeficiency syndrome; AIDS; allergy; autoimmune disease; autoimmune myocarditis; cytostatic; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New T cell binding ligand peptide for treating immunological disorders such as herpes simplex virus, tuberculosis, cancers, acquired immunodeficiency syndrome and allergies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.5%; Score 23; DB 5; Length 10; 100.0%; Pred. No. 1.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                  CEA antigenic peptide C3 associated with cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 27; 110pp; English.
                                                                                       AAU82066 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAY-2001; 2001WO-US016793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAY-2000; 2000US-0206548P.
                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zimmerman DS, Sarin PS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CELS-) CEL-SCI CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-083037/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200189286-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-NOV-2001.
                                                                                                                                                                                                          09-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                            AAU82066;
                                                        AAUH2066
AAU
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(SUMU) SUMITOMO PHARM CO LTD

MO200247474-A1.

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The invention further relates to a novel non-human transgenic mammal transfected with an HLA-A24 gene in which cytotoxic T cells (CTL) are induced by HLA-A24-restricted antigenic stimulation. The invention further relates to a novel method of screening a remedy or a preventitive for a tumour or viral infection charaterised by comprising administering a test substance to the above-described non-human transgenic mammal and then assaying and evaluating whether or not CTLs specific to the test substance are induced therin. The invention also includes: a PSA-origin HLA-A24-restricted tumour antigen peptide selected by this screening method; a chimeric gene useful in forming the above-described transgenic con-human mammal, host cells transformed by this chimeric gene; and cutilisation thereof. The novel non-human transgenic mammal has cytostatic and virucide activity. This sequence represents a human HLA-A24 related peptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.5%; Score 23; DB 7; Lie 100.0%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
Example 9; SEQ ID NO 20; 92pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADG38740 standard; peptide; 10 AA.
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 NGTF 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10 AA;
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Gaps

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4; Conservative

Matches

NGTF 36 NGTF 10

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07-APR-2003; 2003WO-US010571.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                           7
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                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 27
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                                                                                                                                                                                                                                    Producing analogs of Major Histocompatibility Complex (MHC) class I peptidee pytiopes, for treating viral diseases or cancer, comprise producing an analog having (semi)conservative amino acid substitutions of the MHC class I epitope.
                                                                                                                                                                                                                                                                                                          The invention comprises a method for producing a polypeptide that contains an analogue of a major histocompatability complex (MHC) class I peptide epitope, wherein the analogue has enhanced immunogenicity compared to the MHC class I peptide epitope. The method of the invention is useful for producing an analogue or heteroclitic analogue of an MHC class I peptide epitope, and eliciting an immune responses. The method is useful for preparing MHC class I peptide epitope analogues that can be useful for treat viral diseases, cancer and other conditions characterized
                                                                                                                                                                                                                                                                                                                                                                                               by displayed antigens on target cells. The present amino acid sequence represents a peptide of the invention which is derived from human carcinoembryonic antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                major histocompatability complex class I epitope; MHC class I epitope; enhanced immunogenicity; heteroclitic analogue; immune response; viral disease; cancer; human; carcinoembryonic antigen.
major histocompatability complex class I epitope; MHC class I epitope; enhanced immunogenicity; heteroclitic analogue; immune response; viral disease; cancer; human; carcinoembryonic antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.5%; Score 23; DB 7; Length 10; 100.0%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human carcinoembryonic antigen-derived peptide #22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. nc. -
                                                                                                                                                                                                                                                                                      Example 14; SEQ ID NO 178; 244pp; English.
                                                                                                                                                                                             Sette A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADG38664 standard; peptide; 10 AA.
                                                                                                                                                                                             Tangri S,
                                                                                                                  07-APR-2003; 2003WO-US010571
                                                                                                                                        2002US-00116118
2002US-0413471P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
                                                                                                                                                                                            Ishioka G, Fikes J,
                                                                                                                                                                       (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                WPI; 2003-865348/80.
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                                                                         WO2003087126-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10 AA;
                                                     Homo sapiens
                                                                                                                                        05-APR-2002;
26-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                              23-OCT-2003
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                                            Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention comprises a method for producing a polypeptide that contains an analogue of a major histocompatability complex (MHC) class I peptide epitope, wherein the analogue has enhanced immunogenicity compared to the MHC class I peptide epitope. The method of the invention is useful for producing an analogue or heteroclitic analogue of an MHC class I peptide epitope, and eliciting an immune response. The method is useful for preparing MHC class I peptide epitope analogues that can be used to treat viral diseases, cancer and other conditions characterized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by displayed antigens on target cells. The present amino acid sequence represents a peptide of the invention which is derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, mouse, HLA-A24-restricted cancer antigen, antigen, cancer,
tumour suppressor protein, cytostatic, WT1, vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.5%; Score 23; DB 7; Length 10; 100.0%; Pred. No. 1.56+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 14; SEQ ID NO 102; 244pp; English.
                                                                                                                                                                  Sette A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAO24401 standard; peptide; 10 AA.
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                                                                                                                                                              Tangri S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KK.
CO LTD.
05-APR-2002; 2002US-00116118.
26-SEP-2002; 2002US-0413471P.
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20-SEP-2002; 2002JP-00275572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carcinoembryonic antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                the MHC class I epitope
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(SUMU ) SUMITOMO PHARM
(SUGI/) SUGIYAMA H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gotoh M,
                                                                                                                                                              Ishioka G, Fikes J,
                                                                                                 (EPIM-) EPIMMUNE INC.
                                                                                                                                                                                                                              WPI; 2003-865348/80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-090846/09
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Best Local Similarity
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The present invention relates to antigenic peptides derived from tumour suppressor protein WT1 which induce HLA-A24 restricted cytotoxic T-lymphocytes. The peptides can be used in the preparation of cancer vaccine for treatment and prevention of cancer, including leukaemia, multiple myeloma, lymphoma, and cancer of the stomach, colon, breast, liver, ovary, skin, pancreas, prostate and womb. The present sequence is a polypeptide used in the exemplification of the invention
Antigenic peptides derived from WT1 which induce HLA-A24 restricted cytotoxic T-lymphocytes for production of cancer vaccine and treatment and prevention of cancer.
                                                                                                         Disclosure; Page 97; Opp; Japanese
                                                                                                                                                                                                                                                                                                                                                              Sequence 10 AA;
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23.5%; Sco. 100.0%; Pred. No. 0; Mismatches 4; Conservative NGTF 36 NGTF 10 33 Matches ઠ

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Gaps ö

Length 10; 0; Indels

Score 23; DB 8; L Pred. No. 1.5e+02;

Query Match Best Local Similarity

RESULT

ADM12345 standard; peptide; 10 AA (first entry) 20-MAY-2004 ADM12345;

antigen presentation enhancing hybrid polypeptide; mammalian Ii-Key; MHC class II; antibacterial; virucide; fungicide; antirheumatic; antiarthritic; neuroprotective; dermatological; immunosuppressive; antiinflammatory; antidiabetic; antithyroid; immune; rheumatory antiliple sclerosis; lupus erythematosus; diabetes mellitus; myasthenia gravis; autoimmune thyroiditis; scleroderma; dermatomyositis; pemphigus. MHC class I epitope of human carcinoembryonic antigen, 9-5-4.

Homo

US2003235594-A1.

25-DEC-2003.

99US-00396813 14-SEP-1999;

17-SEP-2002; 2002US-00245871

17-JUL-2002; 2002US-00197000.

(ANTI-) ANTIGEN EXPRESS INC

Xu M; Humphreys R,

WPI; 2004-070554/07.

Novel Ii-Key/antigen presentation enhancing hybrid polypeptide, useful for treating infections, rheumatoid arthritis, multiple sclerosis, lupus erythematosus and diabetes mellitus.

Example 9; Page 34; 87pp; English.

polypeptide. The novel polypeptide has an N-terminal element consisting of 4-16 residues of a mammalian Ii-Key peptide and its non-N-terminal deletion modifications, a chemical structure covalently linking the N-terminal element to an MHC class presented epitope of a C-terminal element. The C-terminal element comprises an antigenic epitope, which binds to an antigenic peptide binding site of an MHC class II molecule. The invention relates to a novel antigen presentation enhancing hybrid

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The antigen presentation enhancing hybrid polypeptide has the following activities: antibacterial, virucide, fundicide, antitheunatic, antitheunatic, antitheunatic, neuroprotective, dermachological, immunosuppressive, antiinflammatory, antidiabetic, and antithyroid. The antigen presentation enhancing hybrid polypeptide is useful for modulating the immune response in an individual and for treating infections (such as bacteria, virus, parasite and fungus), rheumatoid arthritis, multiple sclerosis, lupus erythematocous, diabetes mellitus, mysathenia gravis, aucoimmune thyroiditis, scleroderma, dermatomyostits and pemphigus. This sequence represents a mammalian Ii key related peptide epitope of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a non-naturally occurring protein or polypeptide (I) modified by recombinant DNA techniques comprising: a C-terminal element comprising an MHC Class II-presented epitope; an N-terminal element comprising an II-key motif; and an intervening element comprising a sequence of 4-11 amino acid residues where the modification by recombinant DNA techniques taking place within elements (b) and (c). Also
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New non-naturally occurring protein or polypeptide modified by recombinant DNA techniques, useful for treating multiple sclerosis, diabetes mellitus, myasthenia gravis, scleroderma, allergic rhinitis, colltis, cancer or psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carcinoembryonic antigen (CEA) MHC class II-presented epitope #23
                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                 Length 10;
                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                               23.5%; Score 23; DB 8; Le
100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADO38565 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                              4; Conservative
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                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                           Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 29
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directed toward an MHC (major histocompatibility complex) Class II—
C directed toward an MHC (major histocompatibility complex) Class II—
C toward an MHC (lass II—presented epitope of interest comprises; providing a nucleic acid sequence encoding the MHC Class II—presented epitope of interest, the nucleic acid sequence encoding an II—Key motif located 4-II amino acids upstream from the N-terminal residue of the MHC Class II—
C presented epitope of interest, and modifying the II—Key motif located 4-II interest, and modifying the II—Key motif class II—
C interest comprises: providing a nucleic acid sequence encoding the MHC C lass II—Presented epitope of interest, the nucleic acid sequence lacking an II—Key motif located 4-II amino acids upstream from the N-terminal cresting of interest, the MHC Class II—presented epitope of interest, and modifying the N-terminal creating sequence to introduce an II—key motif appropriately content to polypeptide of interest corresponds to a protein or polypeptide of interest corresponds to a protein or polypeptide of interest corresponds to a protein or polypeptide (I) modified by recombinant DNA techniques is useful for treating infectious diseases caused or associated with infection by a content or polypeptide (I) modified by recombinant DNA techniques is useful for treating infectious diseases caused or associated with infection by a content or polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bacterium, virus, paraaite, fungus, ricketteia or other infectious agents. It is also useful for treating rheumatoid arthritis, multiple sclerosis, lupus erythematogus, diabetes mellitus, myasthenia gravis, autoimmune thyroiditis, scleroderma, dermatomyositis, pemphigus, asthma, allergic rhinitis, topical dermatitis, colitis, cancer, psoriasis or adenomas. The present sequence represents the amino acid sequence of carcinoembryonic antigen (CBA) MHC class II-presented epitopeused in the
described are methods for: suppressing or enhancing an immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention.
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23.5%; Score 23; DB 8; Length 10; 100.0%; Prec. ... Query Match Best Local Similarity 100.v. Best-ham 4; Conservative 33 NGTF 36 Sequence 10 AA;

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Gaps ; 0

0; Indels

Pred. No. 1.5e+02;

ADP80010 standard; peptide; 10 AA. (first entry) NGTF 10 18-NOV-2004 ADP80010; ADP80010

1D ADP8

XX ADP8

XX ADP8

XX Huma

XX Huma

XX Homc

XX 8 g

Human HLA-A24 epitope vaccine peptide SeqID265

epitope; HLA-Al; HLA-A2; HLA-A3; HLA-A24; HLA-B7; HLA-B44; tumour associated antigen peptide; cytostatic; vaccine; human.

Homo sapiens

WO2004052917-A2

24-JUN-2004.

10-DEC-2003; 2003WO-US038949.

10-DEC-2002; 2002US-0432017P.

(EPIM-) EPIMMUNE INC.

Fikes JD, Keogh EA,

Southwood S,

Sette A;

WPI; 2004-468809/44.

New HLA-Al, A2, A3, A24, B7 or B44 tumor associated antigen peptides, useful in preparing a composition for diagnosing or treating tumor associated antigen-related disease.

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                                            This invention relates to a novel isolated peptide which comprises at least 1, 2, 3, 4, 5, 6 or 7 epitopes or analogues of the epitopes given in the specification. The peptide comprises HIA-A1, A2, A3, A24, B7 or B44 tumour associated antigen peptide. The invention may be useful for the production of compounds with a cytostatic activity or for the production of a vaccine. The peptide is useful in preparing a composition diagnosing or treating tumour associated antigen-related disease. The present sequence is that of an epitope peptide for use in the peptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide homologue or analogue with constrained conformation - has proline residues flanking the interaction site to impart greater, or more stable,
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Taste modifier peptide, food, drink, sweet, sour, interaction site, constrained conformation, miraculin, curculin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Paste modifier peptide (TM-MIR2) contg. proline brackets.
                                                                                                                                                                                                                                                       Length 10;
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                                                                                                                                                                                                                                                     DB 8; Ler
1.5e+02;
                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                       23.5%; Score 23; 100.0%; Pred. No.
               Claim 1; SEQ ID NO 265; 244pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR67090 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94WO-US004294.
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93US-00143364.
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les 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Evans HJ, Kini RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EVAN/) EVANS H J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KINI/) KINI R M.
                                                                                                                                                                                                                                                                                                                          33 NGTF 36
                                                                                                                                                                                                                                                                                                                                                          NGTF 10
                                                                                                                                                                                                                       Sequence 10 AA;
                                                                                                                                                                                       the invention.
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30-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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Matches
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desirable effects on an interaction site. (Also see AAR67011-88 and AAR67092-152 for analogues of other biologically active peptides contg. an interaction site flanked by conformation constraining gps., eg. RGD peptides.) (Updated on 25-MRN-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G-protein coupled receptor; cardiovascular disease; arrhythmia; myocardial infarction; congestive heart failure; cardiomyopathy; atherosclerosis; arteriosclerosis; embolism; angina; thrombosis; hypertension; Alzheimer's disease; Parkinson's disease; osteoporosis; obesity; human immunodeficiency virus infection; HIV; schizophrenia; sleeplessness; acquired immunodeficiency syndrome; AIDS; leukaemia; sepsis; inflammation; psoriasis; Gaucher's disease; ischaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; immungen; HGPRBMY11; HGPRBMY11v1; HGPRBMY11v2; GPCR74; GPCR81;
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human G-protein coupled receptor HGPRBMY11 polypeptide or polynucleotide, useful for preventing, treating or ameliorating e.g. myocardial infarction, angina, thrombosis, Alzheimer's disease,
                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barber LE;
                                                                                                                                      23.5%; Score 23; DB 2; Length 12; 100.0%; Pred. No. 1.8e+02;
                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human HGPRBMY11 asparagine glycosylation site #1.
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                                                                                                                                                  100.0%; Pred. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ramanathan C,
                                                                                                                                                                                                                                                                                                                                                        ABU11918 standard; peptide; 12 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                schizophrenia, AIDS, leukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-NOV-2000; 2000US-0249613P.
21-DEC-2000; 2000US-0257611P.
16-JUL-2001; 2001US-0305818P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-093137/08.
                                                                                                                                                           Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                  33 NGTF 36
                                                                                                 Sequence 12 AA;
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the method of (8); and (10) screening for candidate compounds capable of binding to and/or modulating activity of a GFCR. The polypeptide or the polymeride to and/or modulating activity of a GFCR. The polypeptide or the polymeride to and/or modulating activity of a GFCR. The polypeptide or the polymeride or distriction, congestive heart failure, arrhythmiss, cardiomyopathy, atherosclerosis, arteriosclerosis, embolism, angina, thrombosis or hypertension). The HGPRBMY11 polypeptide or polymucleotide is also useful for treating, preventing or ameliorating e.g. Alzheimer's disease, parkinson's disease, osteoporosis, obesity, human immunodeficiency virus (HIV) infections, schizophrenia, sepsis, acquired immunodeficiency syndrome (AIDS), leukaemia, sepsis, inflammations, psoriasis, Gaucher's disease or ischeamia (many other cinflammations, psoriasis, Gaucher's disease or ischeamia (many other sequence represents a protein motif or domain of an HGPRBMY11 protein (or variant) which may be used as an immungen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel peptides useful for activating neutrophils or blocking activation of neutrophils, modulating homotypic or heterotypic adhesion of CD66 polypeptides, and modulating immune cell activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is an isolated peptide that was tested for its ability to modulate the function of CD66 family polypeptides and CD66 ligands. 106 sequences of 13 or 14 amino acids in length, and their analogues, were identified that modulate the function of at least one CD66 family polypeptide and/or at least one ligand of the polypeptide. The peptides are capable of modulating activation of neutrophils, activation or inhibition, proliferation and/or differentiation of T-
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD66; CEACAM; adhesion molecule; antiviral; antibacterial; antiinflammatory; cytostatic; neutrophil activation; proliferation; differentiation; cancer; anglogenesis.
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                                                                                                                                                                                                                                                                                                                                                              Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                            23.5%; Score 23; DB 6; Lv
100.0%; Pred. No. 1.8e+02;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-AUG-2000; 2000WO-US023482.
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                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
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(SKUB/) SKUBITZ A P N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD66 peptide CD66c-18.
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                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        NGTF 36
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                                                                                                                                                                                                                                                                                                                         Sequence 12 AA;
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cells, B-cells, NK cells, LAK cells, dendritic cells, or other immune system cells, proliferation and/or differentiation of epithelial cells, homotypic and/or heterotypic adhesion among CD66 family polypeptides and adhesion of CD66 family polypeptides to other ligands. The peptides are useful for delivering a therapeutically active agent to a patient, for modifying the metastasis of malignant cells, for altering bacterial or viral binding to cells or a biomaterial, for altering cell adhesion to a biomaterial, for detecting tumours, for detecting inflammation, for detecting a CD66 protein or its ligand, for altering angiogenesis by contacting endothelial cells, tumour cells or immune cells, for altering an immune response, and for altering keratinocyte proliferation
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Sequence 14 AA;

ö Gaps ö 23.5%; Score 23; DB 4; Length 14; 100.0%; Pred. No. 2.1e+02; 0; Indels 100.0%; Pred. ... 4; Conservative Local Similarity Query Match Matches

NGTF 36 33

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NGTF

AAB88018 standard; peptide; 14 AA.

(first entry) 17-MAY-2001 AAB88018;

CD66 peptide CD66a-18

CD66; CEACAM, adhesion molecule, antiviral, antibacterial, antiinflammatory, cytostatic, neutrophil activation; proliferation, differentiation, cancer, angiogenesis.

Unidentified

WO200113937-A1

25-AUG-2000; 2000WO-US023482. 01-MAR-2001.

99US-0150791P. 26-AUG-1999;

02-SEP-1999;

SKUBITZ K M. SKUBITZ A P N. (SKUB/) (SKUB/)

Skubitz KM, Skubitz APN;

WPI; 2001-234981/24.

Novel peptides useful for activating neutrophils or blocking activation of neutrophils, modulating homotypic or heterotypic adhesion of CD66 polypeptides, and modulating immune cell activation. Claim 1; Page 39; 102pp; English.

The present sequence is an isolated peptide that was tested for its ability to modulate the function of CD66 family polypeptides and CD66 ligands. 106 sequences of 13 or 14 amino acids in length, and their analogues, were identified that modulate the function of at least one CD66 family polypeptide and/or at least one ligand of the polypeptide. The peptides are capable of modulating activation of neutrophils, activation or inhibition, prolliferation and/or differentiation of Testivation or inhibition, prolliferation and/or differentiation of Testivation or inhibition and/or differentiation of Ferentiation of System cells, prolliferation and/or differentiation of epithelial cells, homotypic and/or heterotypic adhesion among CD66 family polypeptides and adhesion of CD66 family polypeptides to other ligands. The peptides are useful for delivering a therapeutically active agent to a patient, for AABB 8018

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modifying the metastasis of malignant cells, for altering bacterial or viral binding to cells or a biomaterial, for altering cell adhesion to a biomaterial, for detecting inflammation, for detecting a CD66 protein or its ligand, for altering angiogenesis by contacting endothelial cells, tumour cells or immune cells, for altering an immune response, and for altering keratinocyte proliferation 8888888

Sequence 14 AA;

Gaps ö DB 4; Length 14; 2.1e+02; 0; Indels 0; Mismatches Score 23; Pred. No. 23.5%; 8 4; Conservative Query Match Best Local Similarity Matches 4; Conserv

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33 NGTF 36 3 NGTF 6 ò

RESULT 35

AAB88099 standard; peptide; 14 AA. AAB88099

AAB88099;

(first entry) 17-MAY-2001

CD66 peptide CD66e-20.

CD66; CEACAM; adhesion molecule; antiviral; antibacterial; antiinflammatory; cytostatic; neutrophil activation; proliferation; differentiation; cancer; anglogenesis.

Unidentified

WO200113937-A1.

01-MAR-2001

25-AUG-2000; 2000WO-US023482.

99US-0150791P. 26-AUG-1999; 02-SEP-1999;

(SKUB/) SKUBITZ K M. (SKUB/) SKUBITZ A P N.

Skubitz APN; Skubitz KM,

WPI; 2001-234981/24.

Novel peptides useful for activating neutrophils or blocking activation of neutrophils, modulating homotypic or heterotypic adhesion of CD66 polypeptides, and modulating immune cell activation.

Claim 1; Page 48; 102pp; English.

The present sequence is an isolated peptide that was tested for its ability to modulate the function of CD66 family polypeptides and CD66 isolands. 106 sequences of 13 or 14 amino acids in length, and their analogues, were identified that modulate the function of at least one compared, were identified that modulate the function of at least one compared, were identified that modulate the function of at least one compared are capable of modulating activation of neutrophils, recitation or inhibition, proliferation and/or differentiation of T-cells, NK cells, LAK cells, dendritic cells, or other immune system cells, proliferation and/or differentiation of Epithablial cells, homotypic and/or heterotypic adhesion among CD66 family polypeptides to other ligands. The peptides are useful for delivaring a therapeutically active agent to a patient, for modifying the metastasis of malignant cells, for altering bacterial or viral binding to cells or a biomaterial, for altering anglogenesis by contacting endothelial cells, tumour cells or immune cells, for altering

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Gaps

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Indels

100.0%; Pred. No. 2.1e+02; ive 0; Mismatches 0;

4; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is an isolated peptide that was tested for its ability to modulate the function of CD66 family polypeptides and CD66 ingands. 106 sequences of 13 or 14 amino acids in length, and their analogues, were identified that modulate the function of at least one companies, were identified that modulate the function of at least one companies, were identified that modulate the function of at least one companies, were identified that modulate the function of the polypeptide. The peptides are capable of modulating activation of neutrophils, activation or inhibition, proliferation and/or differentiation of T-cells, B-cells, NK cells, LAK cells, dendritic cells, or other immune system cells, proliferation and/or differentiation of Equiphelial cells, homotypic and/or heterotypic adhesion among CD66 family polypeptides are adhesion of CD66 family polypeptides to other ligands. The peptides are useful for delivering a therapeutically active agent to a patient, for modifying the metastasis of malignant cells, for altering bacterial or viral binding to cells or mainfant for detecting inflammation, for celtecting andothelial cells, tumoures, for detecting andothelial cells, tumoure of the immune cells, for altering aniespenesis by contacting andothelial cells, tumoure pells or immune cells, for altering an itering an immune response, and for altering keratinocyte proliferation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel peptides useful for activating neutrophils or blocking activation of neutrophils, modulating homotypic or heterotypic adhesion of CD66 polypeptides, and modulating immune cell activation.
                                                                           Gaps
                                                                                                                                                                                                                                                                                           CD66; CEACAM; adhesion molecule; antiviral; antibacterial; antiinflammatory; cytostatic; neutrophil activation; proliferation; differentiation; cancer; angiogenesis.
 an immune response, and for altering keratinocyte proliferation
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                                                Length 14
                                                                        0; Indels
                                               Score 23; DB 4; Le
Pred. No. 2.1e+02;
0; Mismatches 0;
                                      23.5%; Sc.
100.0%; Pred
0; M
                                                                                                                                                                                          AAB88056 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 43; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                         25-AUG-2000; 2000WO-US023482.
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                                                                                                                                                                                                                                           (first entry)
                                   Query Match
Best Local Similarity 100...
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skubitz APN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKUBITZ K M.
SKUBITZ A P N.
                                                                                                                                                                                                                                                                   CD66 peptide CD66b-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-234981/24.
                                                                                                 33 NGTF 36
                                                                                                                           NGTF 6
                         Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                        WO200113937-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                26-AUG-1999;
02-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001
                                                                                                                                                                                                                  AAB88056;
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(SKUB/)
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23.5%; Score 23; DB 4; Length 14;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptide from a surface exposed region of a CD66 family member, useful for modulating the function of CD66 family members, e.g. activation of neutrophils, for treating or diagnosing autoimmune diseases or cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, CD66, CBACAM; cytostatic; antiinflammatory; immunomodulator;
antibacterial; virucide; gene therapy; vaccine; neutrophil;
immune system; autoimmune disease; cancer; infection; bacterial; virus;
inflammatory disease; transplantation; immunisation.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Human CD66 family modulating peptide SEQ ID NO 119.
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100.0%; Pred. No. 2.1e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                             ABP67248 standard; peptide; 14 AA.
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Best Local Similarity
Matches 4; Conserv
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33 NGTF 36
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                                                                                                                                                           RESULT 37
ABP67248
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G-protein coupled receptor; cardiovascular disease; arrhythmia; myocardial infarction; congestive heart failure; cardiomyopathy; atherosclerosis; arreriosclerosis; embolism; angina; thrombosis; hypertension; Alzheimer's disease; Parkinson's disease; osteoporosis; obesity; human immunodeficiency virus infection; HIV; schizophrenia; sleeplessness; acquired immunodeficiency syndrome; AIDS; leukaemia; sepsis; inflammation; psoriasis; Gaucher's disease; ischaemia;
                                                                                                              Human; immungen; HGPRBMY11; HGPRBMY11v1; HGPRBMY11v2; GPCR74; GPCR81;
                                                                                                                                                                                                                                                                                                                                                                                                                                           polynucleotide, useful for preventing, treating or ameliorating e.g. myocardial infarction, angina, thrombosis, Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                              human G-protein coupled receptor HGPRBMY11 polypeptide or
                                                                                                                                                                                                                                                                                                                                                                                     Cacace AM, Barber LE;
                                                                                         Human HGPRBMY11v1 asparagine glycosylation site #1.
                                                                                                                                                                                                                                                                                                                                                                                     Ramanathan C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 79; 444pp; English.
                    ABU11935 standard; peptide; 14 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     schizophrenia, AIDS, leukemia.
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21-DEC-2000; 2000US-0257611P.
16-JUL-2001; 2001US-0305818P.
                                                                                                                                                                                                                                                                                                                                                            (BRIM ) BRISTOL-MYERS SQUIBB
                                                                                                                                                                                                                                                                                         16-NOV-2001; 2001WO-US044019
                                                                  (first entry
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                                                                                                                                                                                                                      Homo sapiens
                                                                   13-FEB-2003
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                                           ABU11935;
RESULT 38
            ABU1193
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The invention relates to an isolated polypeptide (designated HGPRBMYII), which has a G-protein coupled receptor (GPCR) activity (also known as GPCRAL) and is encoded by the CDNA contained in ATCC Deposit Number PTA-2766, its variants (HGPRBMYI1v1 and HGPRBMYI1v2), fragments, domains, species homologues and proteins 95% similar to it. Also included care: (i) the nucleic acids encoding the HGPRBMYII proteins (including variants, fragments, complements and sequences 95% similar to the HGPRBMYII nucleic acids); (2) recombinant vectors; (3) transformed host calls expressing HGPRBMYII; (4) an anti-HGPRBMYII antibody; (5) diagnosing a pathological condition in a subject; (6) identifying an activity in a biological assay; (8) a process for making polymucleotide sequences encoding a gene product condition in a subject; (6) identifying an activity in a biological assay; (8) a process for making polymucleotide sequences encoding a gene product having altered GPCR activity; (9) a shuffled polymucleotide product condition, dor medulating activity; (9) a shuffled polymucleotide or the Dolymucleotide is useful for preventing, treating or ameliorating a medical condition, particularly cardiovascular diseases or disorders, cardiowypathy, atherosclerosis, arteriosclerosis, embolism, angine, thrombosis or hypertension). The HGPRBMYII polypeptide or polymucleotide is also useful for treating, preventing or ameliorating e.g. Alzheimer's diseases. Parkinnon's disease, osteoporosis, acteriosclerosis, embolism, and in immunodeficiency syndrome (AlDS), leukaemia, sepsis, acquired immunodeficiency syndrome (AlDS), leukaemia, sepsis, conflammations, portains, delegaes, osteoporosis, osteoporosis, accomposition or in the specification, congestive disease or ischemia (many other construction may be used as an immungen in the specification). The present construction of an HOPRBMYII protein (or variant) which may be used as an immungen

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The invention relates to an isolated polypeptide (designated HGPRBMY11), which has a G-protein coupled receptor (GPCR) activity (also known as GPCR4 or GPCR81) and is encoded by the CDNA contained in ATCC Deposit Number PTA-2766, its variants (HGPRBMY1101 and HGPRBMY1102), fragments, comparins, species homologues and proteins 95% similar to it. Also included are: (1) the nucleic acids encoding the HGPRBMY11 proteins (including variants, fragments, complements and sequences 95% similar to the HGPRBMY11 mucleic acids); (2) recombinant vectors; (3) transformed host cells expressing HGPRBMY11; (4) an anti-HGPRBMY11 antibody; (5) diagnosing a pathological condition or a susceptibility to a pathological condition or a susceptibility to a pathological condition or a susceptibility to a pathological condition or a susceptibility or a pathological condition or a susceptibility or a pathological condition or a susceptibility or a pathological condition and activity; (9) a shuffled polynucleotide produced by the method of (9); and (10) servening for candidate compounds capable of binding to and/or modulating activity of a GPCR. The polypeptide or the polynucleotide is useful for preventing, treating or ameliorating a
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                                                                                                                                                                                                                                                                                                                                                                                                                                 G-protein coupled receptor; cardiovascular disease; arrhythmia; myozadial infarction; congestive heart failure; cardiomyopathy; atherosclerosis; arteriosclerosis; embolism; angina; thrombosis; hypertension; Alzheimer's disease; Parkinson's disease; osteoporosis; obsetty; human immunodeficiency virus infaction; HIV; schlzophrenia; sleeplessness; acquired immunodeficiency syndrome; AIDS; leukaemia; sepsis; inflammation; psoriasis; Gaucher's disease; ischaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                 Human; immungen; HGPRBMY11; HGPRBMY11v1; HGPRBMY11v2; GPCR74; GPCR81;
                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                        Human HGPRBMY11v1 casein kinase II phosphorylation site #2.
                                    Length 14;
                                                                         Indels
                    DB 6; Le...
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                        23.5%; bcc.
100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                    ABU11953 standard; peptide; 14 AA.
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21-DEC-2000; 2000US-0257611P.
16-JUL-2001; 2001US-0305818P.
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                  Query Match
Best Local Similarity 100.,
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                                                                                                                33 NGTF 36
                                                                                                                                                    NGTF 9
Sequence 14 AA;
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(1) the nucleic acids encoding the HGPRBMY11 proteins (including

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medical condition, particularly cardiovascular diseases or disorders, e.g. myocardial infarction, congestive heart failure, arrhythmias, cardiomyopathy, atherosclerosis, arteriosclerosis, embolism, angina, thrombosis or hypertension). The HGPRBMY11 polypeptide or polymucleotide is also useful for treating, preventing or ameliorating e.g. Alzheimer's disease, Parkinson's disease, osteoporosis, obesity, human immunodeficiency virus (HIV) infections, schizophrenia, sleeplessness, acquired immunodeficiency syndrome (ALDS), leukkaemia, sepsis, inflammations, psoriasis, Gaucher's disease or ischaemia (many other diseases and discorders are listed in the specification). The present sequence represents a protein metif or domain of an HGPRBMY11 protein (or variant) which may be used as an immungen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated polypeptide (designated HGPRBMIII), which has a G-protein coupled receptor (GPCR) activity (also known as PGCR74 or GPCRR), and is encoded by the cDNA contained in ATCC Deposit Number PTA-2766, its variants (HGPRBWIIV1 and HGPRBWYIIV2), fragments, domains, species homologues and proteins 95% similar to it. Also included
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G-protein coupled receptor; cardiovascular disease; arrhythmia; myocadolal infarction; congestive heart failure; cardiomyopathy; atherosclerosis; arteriosclerosis; embolism; angina; thrombosis; hypertension; Alzheimer's disease; Parkinson's disease; osteoporosis; obsesty; human immunodeficiency virus infection; HIV; schlzophrenia; sleeplessness; acquired immunodeficiency syndrome; AIDS; leukaemia; sepsis; inflammation; psoriasis; gaucher's disease; lachaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGPRBMY11; HGPRBMY11v1; HGPRBMY11v2; GPCR74; GPCR81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human HGPRBMY11 N-myristoylation site #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU11944 standard; peptide; 15 AA.
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21-DEC-2000; 2000US-0257611P.
16-JUL-2001; 2001US-0305818P.
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                        NGTF 14
                                                                                                                                                                                                                                                             Sequence 14 AA;
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degenerate, fragments, complements and sequences 95% similar to the cells expressing HQPRBMY11 anti-body; (5) deprending national anti-hQPRBMY11 anti-body; (5) dagnosing a pathological condition or a susceptibility to a pathological condition or a susceptibility to a pathological condition or a subject; (6) identifying a binding partner to the condition in a subject; (7) identifying a binding partner to the condition in a subject; (6) identifying an activity in a biological assay; (8) a process for making polymoclecide sequences encoding a gene product to having altered GPCR activity; (9) a shuffled polymoclecitde produced by the method of (8); and (10) screening for candidate compounds capable of binding to and/or modulating activity of a GPCR. The polymeptide or the collymoclecities is useful for preventing, treating or ameliocating a cardiowascular diseases or disorders, cardiomyopathy, atherosolerosis, arteriosclerosis, embolism, angina, cthrombosis or hypertension). The HCPRBMY11 polypeptide or polymucleotide is also useful for treating, preventing or ameliorating e.g. Alzheimer's disease, parkinson's disease, osteoporosis, obesity, human immunodeficiency virus (HIV) infections, schizophrenia, sleeplessness, acquired immunodeficiency sporiasis, Gusease or ischaemia (many other cinflammations, psoriasis, Gaucher's disease or ischaemia (many other cinflammations, psoriasis, Gaucher's disease or ischaemia (many other capacity which may be used as an immungen of an HGPRBMY11 protein (or variant) which may be used as an immungen
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100.0%; Pred. No. 2.3e+02;
tive 0; Mismatches 0;
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Best Local Similarity 100.
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completed: February 24, 2005, 15:19:36 Search completed: Februs Job time : 130.463 secs

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Similarity 29.2%;
7; Conservative (
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                                                                                                                                                                                                                                                                            US-09-902-540-10583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-902-540-10583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         459
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Best Local S:
Matches 7
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Sequence 13360, A
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
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9, Appli
60291, A
9, Appli
22, Appl
                                                                  February 24, 2005, 15:14:52; Search time 28.2276 Seconds (without alignments) 148.094 Million cell updates/sec
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Sequence 1
Sequence 1
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(/gqn2_6/ptodata/1/iaa/5A_COMB.pep:*

(/gqn2_6/ptodata/1/iaa/5B_COMB.pep:*

(/gqn2_6/ptodata/1/iaa/6A_COMB.pep:*

(/gqn2_6/ptodata/1/iaa/Rea_COMB.pep:*

(/gqn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

(/gqn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-902-540-10583

US-09-902-540-13360

US-08-134-248-7

US-08-614-648B-7

US-08-914-2-648B-7

US-08-913-479-44

US-08-933-402-83

US-08-931-402-83

US-08-931-402-83

US-08-931-497-83

US-08-931-797-83

US-08-931-797-83

US-08-931-797-83

US-08-931-797-83

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US-08-931-797-928-1420

US-09-977-792A-19

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US-09-977-792A-19

US-09-977-792A-19

US-09-977-792A-19

US-09-977-792A-19

US-09-977-792A-19

US-09-350-641C-1420

US-09-350-641C-1420

US-09-350-641C-1420
                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                      513545 seqs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                               US-09-936-956-1
98
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1026
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418
           Copyright
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Match
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                                                                                                                                                                   Scoring table:
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Sequence 1419,
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Sequence 1419,
Sequence 1242,
       US-09-834-784-1419
US-09-515-965A-1419
US-09-350-641A-1419
US-09-350-841A-1419
US-09-082-279B-1242
US-09-314-784-1242
US-09-314-784-1242
US-09-515-965A-1984
US-09-515-965A-1985
US-09-515-965A-1985
US-09-350-641C-1748
US-09-350-641C-1748
US-09-350-641C-1748
US-09-350-641A-1242
US-09-350-841A-1242
US-09-350-841A-1242
US-09-350-841A-1936
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ALIGNMENTS

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Sequence 10583, Application US/09902540
; Sequence 10583, Application US/09902540
; Patent No. 683347
; GRNERAL INPOWENTION;
; APPLICANT: Gladman, Barry S.
; APPLICANT: Gladman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Miegand, Roger C.
; TITLE OF INVENTION: Myxococcue xanthus Genome Sequences and Uses Thereof
; TITLE OF INVENTION: Wyxococcue xanthus Genome Sequences and Uses Thereof
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; WINGER OF SEQ ID NOS: 16825
; SEQ ID NO 10583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-902-540-13360
; Sequence 13360, Application US/09902540
; Sequence 13360, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Wiegend, Roger C.
; APPLICANT: Wiegend, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; TILE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE OF INVENTION: Myxococcus xanthus Genome Sequences
; FILE OF INVENTION: Myxococcus xanthus Yanthus Xanthus Xanthus Xa
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Pred. No. 2.4e+02;
0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 NGTFLDGRQVVQAYLTSGDKVELG 110
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GENERAL INFORMATION:
APPLICANT: Smit, John F.
APPLICANT: Bingle, Wade H.
APPLICANT: Bingle, Wade H.
APPLICANT: No. 6210946ellini, John F.
TITLE OF INVENTION: EXPRESSION AND SECRETION OF HETEROLOGOUS POLYPEPTIDES FROM CAULOR TITLE OF INVENTION: EXPRESSION AND SECRETION OF HETEROLOGOUS POLYPEPTIDES FROM CAULOR CURRENT APPLICATION NUMBER: US/09/142,648B
CURRENT FILING DATE: 1999-03-30
PRIOR FILING DATE: 1997-03-10
PRIOR PILING DATE: 1997-03-10
PRIOR FILING DATE: 1997-03-12
PRIOR FILING DATE: 1996-03-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 1026;
                                                                                      CITY: Boston
STATE: Massachusetts
COMTRY: USA
ZOUTRY: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08106/002001
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                                        3: Fish & Richardson
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1026 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid STRANDEDNESS:
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US-09-142-648B-7
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                                                                                             25.5%; Score 25; DB 4; Length 103; 29.2%; Pred. No. 1.5e+02; tive 0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08194290
Patent No. 5500333
GENERAL INFORMATION:
APPLICANT: Smit, John
AUNGER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ableatager, Arkwright & Garvey
STREET: 3000 South Eads Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Smit, John
APPLICANT: Smit, John
APPLICANT: Bingle, Wade H.
APPLICANT: No. 5976864811ini, John F.
TITLE OF INVENTION: EXPRESSION AND SECRETION OF
TITLE OF INVENTION: HETEROLOGOUS
TITLE OF INVENTION: POLYPEPTIDES FROM CAULOBACTER
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Felease #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/194,290
FILING DATE: 09-FEB-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GAZVEY, GEOFGE A
REGISTRATION NUMBER: 17737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LUDRESS:
STREET: 3000 South Eads Street
CITY: Arington
STATE: Virginia
COUWTRY: USA
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.5%; Score 25; DB 1;
25.0%; Pred. No. 1.6e+03
tive 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 NGTFXXXXXXXXXXXGDXXXXG
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US-08-614-377A-7
; Sequence 7, Application US/08614377A
; Patent No. 5976864
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 59
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 703-836-5288
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
; ORGANISM: Myxococcus xanthus US-09-902-540-13360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1026 amino acids
                                                                                      Query Match
Best Local Similarity 29.2;
Matches 7; Conservative
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Best Local Similarity 25.0
Matches 6; Conservative
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; MOLECULE TYPE: protein
US-08-194-290-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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That Include Conformation-
Groups Which Flank A Protein-Protein Interaction
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                                                                                                                                        COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,222
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 03-MAY-1996
PRIOR APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20007

MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 83, Application US/08933402; Patent No. 594887; GENERAL INFORMATION; GENERAL INFORMATION; TITLE OF INVENTION: Polypeptides That In; TITLE OF INVENTION: Constraining Groups; TITLE OF INVENTION: Site NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS: SOURESPENDINGER ADDRESSE: Foley & Lardner STREET: Suite 500, 3000 K Street NW CONTY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: ISACSON, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 19-SEPP-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
FILING DATE: 29-OCT-1993
                                                                                                        : Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.08;
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Matches 4; Conservative
                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
  Washington
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COUNTRY: USA
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US-08-933-402-83
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Sequence 83, Application US/08934222
Sequence 83, Application US/08934222
Sequence 83, Application US/08934222
Sequence 83, Application US/08934222
Sequence 83, Application Sequence 83, Application:
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: Suite 500, 3000 K Street NW
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                          Gaps
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                                                                                                                                                                                               TITLE OF INVENTION: Nucleic Acids Encoding A Polypeptide TITLE OF INVENTION: Nucleic Acids Encoding A Polypeptide TITLE OF INVENTION: Having Protease Activity NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS: ADDRESSEE: No. 5891701-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.5%; Score 24; DB 2; Length 418; 26.3%; Pred. No. 1.1e+03;
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                        18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FRASESQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,479
FILING DATE: 12-JUN-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: AGIS, Cheryl H
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 5251.000-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
Similarity 25.0%; Pred. No. 1.6e+03; 6; Conservative 0; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                    267 NDTFVAGEVAGAATLTVGDTLSGG 290
                                                            33 NGTFXXXXXXXXXXXX 56
                                                                                                                                                                                                           Sequence 44, Application US/08873479
Patent No. 5891701
GENERAL INFORMATION:
APPLICANT: Sloma, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307 NGTYRVADFSSRGHKTAGD 325
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ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
TYPE: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX:
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 418 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 26.3.
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Best Local Similarity
Matches 6; Conserva
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Sequence 83, Application US/09231797

Patent No. 6084066

GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Proten-Protein Interaction S.
NUMBER OF SEQUENCES. 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                               Sequence 83, Application US/08532818
Sequence 83, Application US/08532818
Patent No. 5965698
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
STREET: Suite 500, 3000 K Street NW
STREET: DESCRIPTION: Street NW
STREET: Since 500, 3000 K Street NW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,818
FLING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04294
FLING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US. 08/143,364
FILING DATE: 29-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US. 08/143,364
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 33,751
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 12 amino acids
amino acid
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Isacson, John P
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 NGTF 36
                                     33 NGTF 36
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; Patent No. 5552465
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ETANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Constraining Groups Which Flank A Proten-Protein Interaction
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
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Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                  23.5%; Score 23; DB 2; Length 12;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/207,621
FILING APPLICATION NUMBER: DCT/US94/04294
FILING DATE: 20-MAY-1996
FILING DATE: 21-APR-1994
FILING DATE: 21-APR-1994
FILING DATE: 23-APR-1994
FILING DATE: 23-APR-1994
FILING DATE: 23-APR-1994
FILING DATE: 23-APR-1994
FILING DATE: 23-APR-1993
FILING DATE: 33-APR-1993

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                       NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILLING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: ISACSON, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 4; Conserv
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US-09-207-621-83
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US-08-933-843-83

Sequence 83, Application US/08933843

Patent No. 6111009

APPLICANT: EVANS, Herbert J.

APPLICANT: EVANS, Herbert J.

APPLICANT: EVANS, Herbert J.

APPLICANT: EVANS, Herbert J.

TITLE OF INVENTION: Site

TITLE OF INVENTION: Site

NUMBER OF SEQUENCES: 153

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: Suite 500, 3000 K Street NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 12;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,843
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DAMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 23-APR-1996
PRIOR APPLICATION NUMBER: U.S. 08/051,741
APPLICATION NUMBER: U.S. 08/051,741
APPLICATION NUMBER: U.S. 08/051,741
APPLICATION ADMART: U.S. 08/051,741
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APPLICALLO.
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION NUMBER: U.S. 08/051,741
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-ARR-1993
ATTORNEY/AGENT INFORMATION:
NAME: ISACGON, JOHN P.
REGISTRATION NUMBER: 33,751
REGISTRATION FOR SEC ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
"""" amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        040433/0148
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REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 04(
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
US-08-934-224-83
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Sequence 83, Application US/08934224

Sequence 83, Application US/08934224

Sequence 83, Application US/08934224

GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, K. Marjunatha
TITLE OF INVENTION: Constraining Groups Which Flank A Protein Interaction
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREE: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/934,224
                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.5%; Scc...
100.0%; Pred. No....
0; Mismatches
                                                                                                                                                                                                                                                                                                FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
PILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
FILING DATE: 21-APR-1994
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA: APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 23-OCT-1993
PRIOR APPLICATION DATA: APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: 18ac80n, John P.
REFERENCE/DOCKET NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 33,751
SEGISTRATION NUMBER: 33,751
Suite 500, 3000 K Street NW
                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                          Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 NGTF 36
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                                                                                               20007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-934-224-83
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Polypeptides That Include Conformation-
Constraining Groups Which Flank A Protein-Protein Interaction
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APPLICANT: Blain, Francoise
APPLICANT: Blain, Francoise
APPLICANT: Bennett, Clark
APPLICANT: Zimmermann, Joseph
APPLICANT: Zimmermann, Joseph
APPLICANT: AppLICANT: Mucleic Acid Sequences And Expression
TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From
TITLE OF INVENTION: Flavobacterium heparinum
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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0
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                                                                                                                                                                                                                                                                                                          COMPUTER: ELADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
COMPUTER: PATENTIAN DATA:
APPLICATION NUMBER: US/09/413,492
FILING DATE: 08/512,818
FILING DATE: 08/512,818
FILING DATE: 21-APR-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 22-CT-1993
PRIOR APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-CCT-1993
PRIOR APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 23-APR-1993
ATTONNINNAMBER: U.S. 08/051,741
APPLICATION NUMBER: U.S. 08/051,741
APPLICATION NUMBER: U.S. 08/051,741
APPLICATION NUMBER: U.S. 08/051,741
APPLICATION NUMBER: U.S. 08/051,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
TITLE OF INVENTION: Polypeptides That:
TITLE OF INVENTION: Constraining Groups
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08258639A
Patent No. 5681733
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania
CITY: Washington, D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 83: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rype: amino acid
ropoLoGY: linear
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                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                     COUNTRY: US
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US-08-934-23-83
US-08-934-223-83
Sequence 83, Application US/08934223
Sequence 83, Application US/08934223
Sequence 84, Application US/08934223
Sequence 87, Application US/08934223
TUTLE OF INVENTION: Constraining Groups Which Flank A Protein Interaction
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCES: 153
CORRESPONDENCES:
ADDRESSEE: FOLEY & Lardner

ADDRESSEE: FOLEY & Lardner

ADDRESSEE: FOLEY & Lardner

ADDRESSEE: FOLEY & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                    DB 3; Length 12; 45;
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                                                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 23; DB 3;
Pred. No. 45;
                                  23.5%; Scor.
100.0%; Pred. No. -c.,
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.5%; Scor.
100.0%; Pred. No. ...
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/522,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIUM DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
PRIUM DATE: 23-APR-1993
ATTONEY/ASENT INFORMATION:
NAME: ISACSON, JOHN P.
REGISTRATION NUMBER: 33,751
REGISTRATION POR SEQ 1D NO: 83:
LENGTH: LEARANTERISTICS:
LENGTH: LEARANTERISTICS:
LENGTH: LEARANTERISTICS:
LENGTH: LENGTH: LEARANTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-413-492-83; Sequence 83, Application US/09413492; Patent No. 6258550; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: EVANS, Herbert J.
                                               Query Match 23.5
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                             33 NGTF 36
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: IDEX TECHNOLOGIES and
APPLICANT: ZIMMERNANN, Joseph
TITLE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From
TITLE OF INVENTION: Flavobacterium heparinum
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                  ö
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Patent No. 6703491
GENERAL INFORMATION
THORMATION SET APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REPERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 60291
LENGTH: 23
                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                  Length 23;
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CURRENT APPLICATION DATA:
APPLICATION VMBER: PCT/US95/07391A
FILING DATE: 09-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
89;
                                                                                                                                                                DB 2;
89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington, D.C.
COUNTRY: U.S.A.
ZIP: 20004.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                             23.5%; Score 23; DB 100.0%; Pred. No. 89; ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.5%; Score 23; DB 100.0%; Pred. No. 89; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Xaa means any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/258,639
FILING DATE: 10 JUNE 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Drosophila melanogaster
                                                                                                                                       Query Match
Best Local Similarity luv...
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity luv...
A; Conservative
                           23 amino acids
SEQUENCE CHARACTERISTICS
                                                                                          ; MOLECULE TYPE: peptide US-08-900-951-9
                                             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                               33 NGTF 36
                                                                                                                                                                                                                                                                                                            16 NGTF 19
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US-09-270-767-60291
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PCT-US95-07391A-9
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APPLICANT: Su, Hongsheng
APPLICANT: Blain, Francoise
APPLICANT: Bennett, Clark
APPLICANT: Gu, Kangfu
APPLICANT: Zimmermann, Joseph
APPLICANT: Zimmermann, Joseph
APPLICANT: Zimmermann, Joseph
APPLICANT: Systems For Heparinase II And Heparinase III Derived From
ITILE OF INVENTION: Systems For Heparinase II And Heparinase III Derived From
ITILE OF INVENTION: Flavobacterium heparinum
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Parter:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                         CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/258,639A

FILING DATE: 10 JUNE 1994

CLASSIFICATION: 435

ATTONENY/AGENT INFORMATION:

NAME: Healey, William J.

REGISTRATION NUMBER: 36,160

REGISTRATION NUMBER: 36,160

REGISTRATION NUMBER: 36,160

TELEPHONE: (202)942-8400

TELEPHONE: (202)942-8400

TELEPRATION FOR SEQ ID NO: 9: SEQUENCE CHRAACTERISTICS: (202)942-8400

INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHRAACTERISTICS: (202)942-8400

TELEPHONE: (202)942-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CIP: 2004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/900,951
FILING DATE: US/08/900,951
FILING APPLICATION NUMBER: 08/258,639
FILING DATE: 10 JUNE 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.5%; Scc. 100.0%; Pred. No. c. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1455 Pennsylvania Avenue, N.W. CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Healey, William J.
REGISTATION NUMBER: 36,160
REFERENCE, DOCKET NUMBER: 104385.116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (2029) 942 8460
TELEFAX: (202) 942 8484
INFORMATION FOR SEQ 1D NO: 9:
                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 NGTF 36
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MEDIUM TYPE:
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APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Meruka, G.
APPLICANT: Meruka, G.
APPLICANT: Meruka, G.
APPLICANT: Amwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT TAILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                               Length 31;
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; Patent No. 625879E
; Patent No. 625879E
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Lambert, Mohmed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: PHARNACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICANTON: PHARNACOKINETIC PROPERTIES
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1420
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                                                                                            Query Match 23.5%; Score 23; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0;
                           CTHER INFORMATION: Synthetic Construct US-09-997-792A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-315-304B-1420
; Sequence 1420, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
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      ; FEATURE:
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                                                                                                                                                                                                                                                                                                                                            23.5%; Score 23; DB 5; Length 23; 100.0%; Pred. No. 89; 0; Indels tive 0; Mismatches 0; Indels
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US-09-997-792A-19
; Sequence 19, Application US/0997792A
; Patent NO. 655521
; GENERAL INFORMATION:
; APPLICANT: ELI LILLY and COMPANY
; TILL OF INVENTION: Glucagon-Like Peptide-1 Crystals
; TILL OF INVENTION: Glucagon-Like Peptide-1 Crystals
; TILL OF INVENTION: CA10242A
; CURRENT APPLICATION NUMBER: US/09/997,792A
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US 60/069,728
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 19
; LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22, Application US/09209799D

Patent No. 6380357

GENERAL INFORMATION

APPLICANT: Horfmann, James

APPLICANT: Hoffmann, James

APPLICANT: Narasinhan, Chakravarthy

TITLE OF INVENTION UNMER: US/09/209, 799D

CURRENT FILING DATE: 1998-12-11

NUMBER OF SEQ ID NOS: 29

SOFTWARER: Patentin version 3.0

LENGTH: 31

LENGTH: 31
ATTORNEY/AGENT INFORMATION:

NAME: BAKER, Hollie L.

REGISTRATION NUMBER: 31,321

REFERENCE/DOCKET NUMBER: 104385.116PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)942-8484

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: synthetic construct
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Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
MULECULE TYPE: peptide
PCT-US95-07391A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial
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RESULT 27
US-09-350-841A-1420
; Sequence 1420, Application US/09350841A
; Patent No. 6750008
; GENERAL INFORMATION:
; AFPILGANT: Jeffs, Peter;
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: PUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; FILE REPRENCE: 7872-066-999
; CURRENT APPLICATION UMBER: US/09/350,841A
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 1946
; SOFTWARE: PATENTIN Ver. 2.1
; SEQ ID NO 1420
                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Guthrie, K.
APPLICANT: Meruka, G.
APPLICANT: Meruka, G.
APPLICANT: Amwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYBEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-067
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-067
CURRENT FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOUTHARE: PastSEQ for Windows Version 3.0
SEQ ID NO 1420.
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                                           Length 38;
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 23.5%; Score 23; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0;
                                             Score 23; DB 4; L
Pred. No. 1.5e+02;
                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                         Sequence 1420, Application US/09350641C Patent No. 6656906 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTHER INFORMATION: Core polypeptide US-09-350-841A-1420
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                                             23.5%;
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ORGANISM: Artificial Sequence
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                                        Query Match
Best Local Similarity 100.
Matches 4; Conservative
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US-09-515-965A-1420
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Sequence 1420, Application US/09515965A

Patent No. 6623741

GENERAL INFORMATION:
APPLICANT: Delimedico, M.
APPLICANT: Delimedico, M.
APPLICANT: Lambert, D.
APPLICANT: Lambert, D.
APPLICANT: Sista, P.
TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUILDS APPLICANT: 1912.073
CURRENT APPLICATION NUMBER: US/09/515,965A
CURRENT FILING DATE: 12999-05-20
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20

NUMBER OF SEQ ID NOS: 1994
SOFTWARE FREESEQ for Windows Version 3.0
SEQ ID NO 1420
LENGTH: 38
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                23.5%; Score 23; DB 3; Length 38; 100.0%; Pred. No. 1.5e+02; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                          Sequence 1420, Application US/09834784

Sequence 1420, Application US/09834784

GENERAL INPORMATION:
APPLICANT: Barney, Skally
APPLICANT: Genthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohmed
APPLICANT: Merutka, Dennis
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT APPLICATION NUMBER: 09/082,279
PRIOR PILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: PRESENCE 1515
LENGTH 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Core polypeptide US-09-834-784-1420
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OTHER INFORMATION: Core polypeptide
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 4; Conservative
                Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                           33 NGTF 36
                                                                                                                                                        12 NGTF 15
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US-09-515-965A-1420
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# PAPLICANT: Antcaak, J.
# APPLICANT: Antcaak, J.
# APPLICANT: Antcaak, J.
# APPLICANT: Antcaak, J.
# APPLICANT: Belwedico, M.
# APPLICANT: Lambert, D.
# APPLICANT: Lambert, D.
# APPLICANT: Lambert, D.
# APPLICANT: Sista, P.
# TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
# TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
# TILE REFERENCE: 7872-073
# CURRENT APPLICATION NUMBER: 108/09/515,965A
# CURRENT FILING DATE: 1999-05-20
# PRIOR FILING DATE: 1999-05-20
# PRIOR FILING DATE: 1998-05-20
# NUMBER OF SEQ ID NOS: 1994
# SOFTWARE: FastSEQ for Windows Version 3.0
# SEQ ID NO 1419
# LENGTH: 39
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; Sequence 1419, Application US/09834784
; Patent No. 6562787
; GENERAL INPORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Merutxa, Gene
; APPLICANT: Merutxa, Gene
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACCKINETIC PROPERTIES
; TITLE OF INVENTION: PHARMACCKINETIC PROPERTIES
; TITLE OF SEPLICATION NUMBER: US/09/834,784
; CURRENT PILING DATE: 2001-04-13
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF ERQ ID NOS: 1515
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1419
; LENGTH: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 23.5%; Score 23; DB 4; Le Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 4; Conservative 0; Mismatches 0;
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; Sequence 1419, Application US/09515965A
; Patent No. 6623741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: Core polypeptide US-09-834-784-1419
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14 NGTF 17
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APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REPERENCE: 7872-052
FURRENT PELICATION NUMBER: 09/082,279
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR PELICATION DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 119
LENGTH: 39
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                                                                                                                                                                        Sequence 119, Application US/09082279B
Sequence 119, Application US/09082279B
Sequence No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Anwer, Mohmed
APPLICANT: Anwer, Mohmed
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
FILE REFERENCE: 7872-043
CURRENT APPLICANTON NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1419
LENGTH: 39
LENGTH: 39
LENGTH: 39
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US-09-082-279B-1419
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
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                      33 NGTF 36
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US-09-082-279B-1419
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US-09-315-304B-1419
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APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Meruka, G.
APPLICANT: Ameruka, G.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYRDID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-652
CURRENT TILING DATE: 1999-05-20
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1242
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           Sequence 1242, Application US/09082279B

Patent No. 6258782

GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Anwer, Mohmed
APPLICANT: Anwer, Mohmed
APPLICANT: Anwer, Mohmed
APPLICANT: Anwer, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
FILE REFERENCE: 7872-043
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FREUSEQ for Windows Version 3.0
SEQ ID NO 1242
LENTH: 40
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Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 4; Conservative 0; Mismatches 0;
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, OTHER INFORMATION: Core polypeptide
US-09-315-304B-1242
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23.5%;
Best Local Similarity 100.0%;
Matches 4; Conservative 0
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   US-09-082-279B-1242
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US-09-834-784-1242
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Patent No. 675008
GENERAL INFORMATION
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
FILLE REFERENCE: 7872-066-999
CURRENT APPLICATION NUMBER: US/09/350,841A
CURRENT PILLING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 1946
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 1419
LENGTH: 39
                                                                                                                                                                                                                                                                                                         APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Merutka, G.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRE: US/09/350,641C
CURRENT APPLICATION NUMBER: US/09/350,641C
CURRENT FILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
PRIOR PLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1999-05-20
PRIOR FLING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: PARLSEQ for Windows Version 3.0
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100.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 0;
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Patent No. 6656906
GENERAL INFORMATION:
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; OTHER INFORMATION: Core polypeptide
US-09-350-841A-1419
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 4; Conservative
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Matches 4; Conservative
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14 NGTF 17
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LENGTH: 39
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Sequence 1985, Application US/09515965A
; Sequence 1985, Application US/09515965A
; Patent No. 6623741
; GENERAL INFORMATION:
APPLICANT: Bollmedico, M.
APPLICANT: Lambert, D.
APPLICANT: Lambert, D.
APPLICANT: Lambert, D.
TITLE OF INVENTION: ASSOLATED EVENTS INCLUDING RSV TRANSMISSION
TITLE OF INVENTION: ASSOLATED EVENTS INCLUDING RSV TRANSMISSION
FILE REFERENCE: 7872-073
CURRENT PLIJNG DATE: 2000-02-29
FRIOR PLIJNG DATE: 2999-05-20
FRIOR PLIJNG DATE: 1999-05-20
FRIOR PLIJNG DATE: 1999-05-20
FRIOR FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 1994
SOFTWARE: FREESEQ for Windows Version 3.0
SEQ ID NO 1985
LIENTHS.
                         APPLICANT: Antczak, J.
APPLICANT: Delmedico, M.
APPLICANT: Delmedico, M.
APPLICANT: Delmedico, M.
APPLICANT: Erickon, J.
APPLICANT: Exercity D.
APPLICANT: Lambert, D.
APPLICANT: Sista, P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
FILE REFERENCE: 782-073
CURRENT APPLICATION NUMBER: US/09/515,965A
CURRENT PILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR APPLICATION NUMBER: 09/082,279
NUMBER: OF SEQ ID NOS: 1994
SOUTWARE: FRAESEQ for Windows Version 3.0
ERGOID NO 1984
LENGTH: 40
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1.6e+02;
thes 0; Indels
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LOCATION: 4, 8
OTHER INFORMATION: Xaa = Abu (aminobutyric acid)
US-09-515-965A-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.5%; Score 23; DB 100.0%; Pred. No. 1.6 tive 0; Mismatches
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Best Local Similarity 100.9
Matches 4, Conservative
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APPLICANT: Antecaak, J.
APPLICANT: Delmedico, M.
APPLICANT: Delmedico, M.
APPLICANT: Delmedico, M.
APPLICANT: Delmedico, M.
APPLICANT: Sista, P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
FILE REFERENCE: 7872-073
CURRENT APPLICATION NUMBER: US/09/515,965A
CURRENT FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/15,304
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR PILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1994
SOFTWARE: FASESEQ for Windows Version 3.0
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                                                                                               APPLICANT: Anwer, Mohmed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACCKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastEGQ for Windows Version 3.0
SEQ ID NO 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
23.5%; Score 23; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0;
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US-09-515-965A-1984
; Sequence 1984, Application US/09515965A
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. Sequence 1242, Application US/09515965A

. Patent No. 6623741

. GENERAL INFORMATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Core polypeptide
US-09-834-784-1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 4; Conservative
Barney, Shawn
Guthrie, Kelly
Merutka, Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 NGTF 36
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LENGTH: 40
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14 NGTF 17

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RESULT 40

US-09-350-641C-1242

i Sequence 1242, Application US/09350641C

i Patent No. 6656906

i GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Merutka, G.

APPLICANT: Anwer, M.

CURRENT APPLICATION NUMBER: US/09/350,641C

CURRENT APPLICATION NUMBER: 09/082,279

PRIOR PLING DATE: 1998-05-20

PRIOR PLING DATE: 1998-05-20

PRIOR PLING DATE: 1998-05-20

PRIOR PLING DATE: 1998-05-30

PRIOR PLING DATE: 1998-05-30

PRIOR PLING DATE: 1998-05-30

ANWER OF SEC ID NOS: 1757

SOFTWARE: FASTESC for Windows Version 3.0

TYPE: PRT

CORRENT: Artificial Sequence

TYPE: PRT

COTHER INFORMATION: Core polypeptide

US-09-350-641C-1242
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Best Local Similarity 100.
Matches 4; Conservative
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Search completed: February 24, 2005, 15:25:30 Job time : 30.2276 secs

33 NGTF 36

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14 NGTF 17

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GenCore version 5.1.6
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Pebruary 24, 2005, 15:23:51 ; Search time 81.0406 Seconds
(without alignments)
226.127 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-09-936-956-1 98 Title: Perfect score:

Scoring table: Sequence:

1380268 seqs, 327241040 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 248, App	Sequence 252, App	Sequence 250, App	Sequence 7, Appli	Sequence 7, Appli	Sequence 1, Appli	Sequence 194, App	Sequence 305, App	Sequence 48, Appl	Sequence 305, App	Sequence 23, Appl	Sequence 23, Appl	Sequence 42, Appl
	ΩI	US-10-652-870-248	US-10-652-870-252	US-10-652-870-250	US-09-379-931-7	US-10-223-597-7	US-10-478-676-1	US-10-657-022-194	US-10-245-871-305	US-10-296-317-48	US-10-253-286-305	US-09-991-225-23	US-10-369-405-23	US-09-991-225-42
	98	16	16	16		14	17	16	15	15	15.	10	15	10
	Query Match Length DB ID	260	260	261	1026	1026	1026	6	10	10	10	12	12	14
ф	Query Match	25.5	25.5	25.5	25.5	25.5	25.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5
	Score	25	25	25	25	25	25	23	23	23	23	23	23	23
	Result No.	-	7	٣	4	2	9	7	80	0	10	11	12	13

69, 69, 72, 2046	606, 606, 606, 312,	Sequence 5 Sequence 15 Sequence 16 Sequence 22, Sequence 5,	Sequence 1113, App Sequence 1420, Ap Sequence 1419, Ap Sequence 1242, Ap Sequence 1747, Ap Sequence 1748, Ap	00000
US-10-369-405 US-10-369-405 US-10-369-405 US-09-991-225 US-09-991-225	US-10-369-405- US-10-369-405- US-09-958-405- US-10-253-471- US-10-253-493- US-10-253-493- US-10-253-286-	US-10-296-317- US-10-296-317- US-10-424-599- US-09-209-7990- US-09-736-960-5 US-09-736-960-5	US-03-995-494-113 US-10-351-641-1420 US-10-351-641-1419 US-10-351-641-1242 US-10-351-641-1747 US-10-351-641-1748 US-03-912-628-9	US-10-116-166 US-10-425-114 US-10-351-641 US-10-437-963 US-10-424-599
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ALIGNMENTS

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sequence 248, Application US/10652870

sequence 248, Applicant Electric Leah

septicant Telecher, Leah

septicant Bernfield, Liesel

septicant Bernfield, Liese
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Gaps ö Query Match 25.5%; Score 25; DB 16; Length 260; Best Local Similarity 25.0%; Pred. No. 1.2e+03; Matches 6; Conservative 0; Mismatches 18; Indels

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APPLICANT: Smit, John
APPLICANT: Bingle, Wade H.
TITLE OF INVENTION: EXPRESSION AND SECRETION OF HETEROLOGOUS POLYPEPTIDES FROM CAULO:
FILE REFRENCE: 08106/002003
CURRENT APPLICATION NUMBER: US/09/379,931
CURRENT FILING DATE: 1995-08-24
PRIOR APPLICATION NUMBER: US 08/194,290
PRIOR APPLICATION NUMBER: US 08/194,290
PRIOR PILING DATE: 1994-02-09
PRIOR PELING DATE: 1994-02-09
PRIOR PELING DATE: 1992-06-09
PRIOR PELING DATE: 1992-06-09
PRIOR FILING DATE: 1992-06-09
SPRIOR FILING DATE: 1992-06-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Smit, John
APPLICANT: Bingle, Wade H.
APPLICANT: Bingle, Wade H.
APPLICANT: Bingle, Wade H.
APPLICANT: No. US2003135037A1ellini, John F.
TITLE OF INVENTION: EXPRESSION AND SECRETION OF HETEROLOGOUS POLYPEPTIDES FROM CAULOBY, FILE REFERENCE: 08106/00203
CURRENT PELLING DATE: 202-08-19
CURRENT PILING DATE: 1999-08-24
FRIOR REPLICATION NUMBER: US/09/379, 931
PRIOR PILING DATE: 1996-03-12
PRIOR FILING DATE: 1996-03-12
PRIOR FILING DATE: 1996-03-12
PRIOR PLILING DATE: 1996-03-12
PRIOR PLILING DATE: 1996-03-12
PRIOR PLILING DATE: 1996-03-12
PRIOR PLILING DATE: 1996-03-13
PRIOR PLILING DATE: 1992-06-09
SPRIOR FILING DATE: 1992-06-09
SPRIOR PLILING DATE: 1992-06-09
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25.5%; Score 25; DB 9; I
Best Local Similarity 25.0%; Pred. No. 4.5e+03;
Matches 6; Conservative 0; Mismatches 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/10223597
Publication No. US20030135037A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-478-676-1; Sequence 1. Application US/10478676; Publication No. US20550032194A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Caulobacter crescentus
US-09-379-931-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Caulobacter crescentus
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Publication No. US20040167068A1

GENERAL INPORMATION:
APPLICANT: Fletcher, Leah
APPLICANT: Fletcher, Leah
APPLICANT: John, Farley
APPLICANT: John, Farley
APPLICANT: John, Farley
APPLICANT: Metchiadin
TILE OF INVENTION: Meningococcal Disease
FILE REFERENCE: 38523.00026
CURRENT APPLICATION NUMBER: US/10/652,870
FRIOR PILL APPLICATION NUMBER: US/10/652,870
PRIOR FILING DATE: 2003-09-02
SUNBER OF SEQ ID NOS: 329
SUNBER OF SEQ ID NOS: 329
                                                                                                                                APPLICANT: Zlotnick, Gary
APPLICANT: Zlotnick, Gary
APPLICANT: Zlotnick, Cary
APPLICANT: Zlotnick, Carley
APPLICANT: Bernield, Liesel
APPLICANT: Bercalf, Benjamin
TITLE OF INVENTION: Movel Immunogenic Compositions for the Prevention and Treatment of INVENTION: Normal Immunogenic Compositions for the Prevention and Treatment of INVENTION: Movel Immunogenic Compositions for the Prevention and Treatment of INVENTION: NORMBER: US/10/652,870
PRIOR APPLICATION NUMBER: US 10/652,870
PRIOR APPLICATION NUMBER: US 10/652,870
NUMBER OF SEQ ID NOS: 329
NUMBER OF SEQ ID NOS: 329
SOFTWARE: Patentin version 3.1
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Best Local Similarity 25.0%; Pred. No. 1.2e+03; Matches 6; Conservative 0; Mismatches 18; Indels
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                           ; Sequence 252, Application US/10652870; Publication No. US20040167068A1; GENERAL INFORMATION:
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; Patent No. US20020009792A1
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ORGANISM: Neisseria meningitidis
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ORGANISM: Neisseria meningitidis
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US-10-652-870-250
US-10-652-870-252
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LENGTH: 260
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LENGTH: 261
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US-09-379-931-7
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33 NGTF 36
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Sequence 305, Application US/10245871
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU MINZHEN
TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2013
CURRENT APPLICATION NUMBER: US/10/245,871
CURRENT PILING DATE: 2003-01-09
PRIOR PILING DATE: 2002-07-17
                              APPLICANT: BUNGLE, wade, H.

TITLE OF INVENTION: PROTEASE DEFICIENT CAULOBACTER HOST CELLS
FILE REFERENCE: 3225-199048

CURRENT APPLICATION NUMBER: US/10/478,676

CURRENT FILING DATE: 2003-11-24

PRIOR FILING DATE: 2002-05-22

PRIOR FILING DATE: 2002-05-22

PRIOR FILING DATE: 2001-05-22

PRIOR FILING DATE: 2001-05-22

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin version 3.1

SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 194, Application US/10657022

Publication No. US20040180354A1

GENERAL INFORMATION:
APPLICANT: Simard, John J. L.
APPLICANT: Diamond, David C.
APPLICANT: Liu, Liping
APPLICANT: Liu, Liping
TITLE OF INVENTION: EPITOPE SEQUENCES
FILE REFRENCE: MANK. 032A
CURRENT APPLICATION NUMBER: US/10/657,022
CURRENT PELING DATE: 2003-09-04

PRIOR PILING DATE: 2003-09-06

NUMBER OF SEQ ID NOS: 610

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 194
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; ORGANISM: Caulobacter crescentus
US-10-478-676-1
                      NOMELLINI, John, F.
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Best Local Similarity
Matches 6; Conserva
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US-10-657-022-194
APPLICANT: SMIT, John
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US-10-245-871-305
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Sequence 305, Application US/10253286

Publication No. US2004005881A1

GENERAL INFORMATION:

APPLICANT: HUMPHREYS, ROBERT

APPLICANT: HUMPHREYS, ROBERT

TITLE OF INVENTION: I1-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES

FILE REPREBENCE: EMH-2015

CURRENT APPLICATION NUMBER: 10/197,000

PRIOR PILING DATE: 2003-01-13

PRIOR PLING DATE: 2003-07-17

PRIOR PLING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 905

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 305

LENGTH: 10
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Sequence 48, Application US/10296317

Sequence 48, Application US/10296317

Sequence 48, Application US/10296317

Sublication No. UG20040057968A1

Seneral Information: Calcorp

APPLICANT: Calcorp

APPLICANT: Sarin, Daniel S

APPLICANT: Sarin, Prem S

TILLE OF INVENTION: T CELL BINDING LIGAND PEPTIDE

FILE REFERENCE: C3-12

CURRENT APPLICATION UNBER: US/10/296,317

CURRENT FILING DATE: 2002-01-122

PRIOR APPLICATION NUMBER: DG2-11-22

PRIOR PLING DATE: 2000-05-24

PRIOR APPLICATION NUMBER: PCT/US07/16793

PRIOR PLING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 96

SOFTWARE: PatentIn version 3.1

SEQ ID NO 48
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PRIOR APPLICATION NUMBER: 09/396,813 PRIOR FILING DATE: 1999-09-14 NUMBER OF SEQ ID NOS: 905 SOFTWARE: PATENTIN Ver. 2.1 SEQ ID NO 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: CEA Peptide C3
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 4; Conservative
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; ORGANISM: Homo sapiens
US-10-245-871-305
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NGSOUL 12.25-42

1 Sequence 42, Application US/0991225

2 Sequence 42, Application US/0991225

3 Sequence 42, Application US/0991225

3 GENERAL INPORMATION:

4 APPLICANT: Brietol-Myers Squibb Company

5 TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, EXPRESSED HI

7 TITLE OF INVENTION: HEART AND VARIANTS THEREOF

7 TITLE OF INVENTION: HOWBER: US/09/991,225

7 CURRENT APPLICATION NUMBER: 60/249,613

PRIOR PILING DATE: 2000-11-17

PRIOR APPLICATION NUMBER: 60/257,611

PRIOR FILING DATE: 2000-12-21

PRIOR FILING DATE: 2001-11-6

PRIOR FILING DATE: 2001-11-6

NUMBER OF SEQ ID NOS: 81

5 SEQ ID NO 4:

LENGTH: 14
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                         Length 12;
                                                                           Indels
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US-09-991-225-69

i Sequence 69, Application US/09991225

i Publication No. US20030153063A1

i GENERAL INFORMATION:

APPLICANT: BITSIGLO-Myers Squibb Company

TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED

TITLE OF INVENTION: HEART AND VARIANTS THEREOF

FILER REFERENCE: D0075.NP

CURRENT APPLICATION NUMBER: US/09/991,225

CURRENT APPLICATION NUMBER: 60/249,613

PRIOR APPLICATION NUMBER: 60/249,613

PRIOR PILING DATE: 2000-11-17

PRIOR FILING DATE: 2000-11-17

PRIOR FILING DATE: 2000-12-21

PRIOR FILING DATE: 2001-11-16

NUMBER OF SEQ ID NOS: 81

SOFTWARE: PATCHIN VERSION 3.0

SEQ ID NO 69

LENGTH: 14

TYPE: PRT
                       Query Match 23.5%; Score 23; DB 15; I
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0;
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, ORGANISM: Homo sapiens
US-09-991-225-42
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US-09-991-225-69
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US-10-369-405-23

US-10-369-405-23

Sequence 23, Application US/10369405

Publication No. US2003224400A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPREMYII, AND VARIANTS

TITLE OF INVENTION: THEREOF

FILE REFERRANCE: D0075A CIP

CURRENT APPLICATION NUMBER: US. 60/249,613

PRIOR PELING DATE: 2000-11-17

PRIOR PELING DATE: 2000-11-16

PRIOR PELING DATE: 2000-11-16

PRIOR PELING DATE: 2000-11-16

PRIOR PELING DATE: 2000-1-21

PRIOR PELING DATE: 2000-1-21

PRIOR PELING DATE: 2000-10-71

PRIOR PELING DATE: 2000-10-71

PRIOR PELING DATE: 2000-10-21

PRIOR PELING DATE: 2001-07-16

NUMBER OF SEQ ID NOS: 94

SOFTWARE: PatentIn version 3.2

SEQ ID NO 23

LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bristol-Wyers Squibb Company
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, EXPRESSED HI
TITLE OF INVENTION: HERAT AND VARIANTS THEREOF
FILE REFERENCE: D0075.NP
CURRENT APPLICATION NUMBER: US/09/991,225
CURRENT FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: 60/249,613
PRIOR APPLICATION NUMBER: 60/249,613
PRIOR PILING DATE: 2000-11-7
PRIOR APPLICATION NUMBER: 60/257,611
PRIOR APPLICATION NUMBER: 60/357,611
PRIOR APPLICATION NUMBER: 60/357,611
PRIOR PILING DATE: 2001-07-16
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
SEQ ID NO 23
LENGTH: 12
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                                                                                                  23.5%; Score 23; DB 15; Length 10; 100.0%; Pred. No. 1.4e+02; cive 0; Mismatches 0; Indels
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Pred. No. 1.7e+02;
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                Query Match 23.5
Best Local Similarity 100.
Matches 4; Conservative
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Matches 4; Conservative
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-253-286-305
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CRGANISM: homo sapiens
US-09-991-225-23
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US-09-991-225-23
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Sequence 60, Application US/09991225

Sequence 60, Application US/09991225

Sequence 60, Application US_0030153063A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, EXPRESSED HIGHTLE OF INVENTION: HEART AND VARIANTS THEREOF

TITLE OF INVENTION: HEART AND VARIANTS THEREOF

FILE REFERENCE: D0075.NP

CURRENT PELLING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/249,613

PRIOR APPLICATION NUMBER: 60/257,611

PRIOR APPLICATION NUMBER: 60/205,818

PRIOR APPLICATION NUMBER: 60/205,818

PRIOR PILING DATE: 2000-10-16

NUMBER OF SEQ 1D NOS: 81

SOFTWARE: Patentin version 3.0

LENGTH. 15
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Sequence 72, Application US/09991225

Sequence 72, Application US/09991225

Sequence 72, Application US/09991225

Sequence 72, Application Wo. US203015306341

GENERAL INFORMATION:

TITLE OF INVENTION: HEART AND VARIANTS THEREOF

TITLE OF INVENTION: HEART AND VARIANTS THEREOF

TITLE OF INVENTION: HEART AND VARIANTS THEREOF

TITLE OF INVENTION: HUMBER: US/09/991,225

CURRENT FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/249,613

PRIOR APPLICATION NUMBER: 60/257,611

PRIOR APPLICATION NUMBER: 60/257,611

PRIOR APPLICATION NUMBER: 60/257,611

PRIOR APPLICATION NUMBER: 60/257,611

PRIOR APPLICATION NUMBER: 60/305,818

PRIOR FILING DATE: 2001-07-16

NUMBER OF SEQ ID NOS: 81

SEQ ID NO 72

LENGTH: 15
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Pred. No. 2.1e+02;
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llarity 100.0%;
Conservative 0
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Best Local Similarity 100.
Matches 4; Conservative
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US-09-991-225-60
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US-09-991-225-72
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Best Local Similarity
Matches 4; Conserv
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11 NGTF 14
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                                    셤
                                                                                                                                                                                                            ## Sequence 42, Application US/10369405
## Sequence 42, Application US/10369405
## Sequence 42, Application No. US20030224400A1
## GENERAL INFORMATION:
## APPLICANT: Bristol-Myers Squibb Company
## TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, AND VARIANTS
## TITLE OF INVENTION: THEREOF
## CURRENT APPLICATION NUMBER: US/10/369,405
## CURRENT APPLICATION NUMBER: U.S. 60/249,613
## PRIOR PLING DATE: 2000-11-17
## PRIOR PLING DATE: 2000-11-17
## PRIOR PLING DATE: 2000-12-21
## PRIOR PLING DATE: 2000-12-21
## PRIOR APPLICATION NUMBER: U.S. 60/257,611
## PRIOR PLING DATE: 2000-10-16
## PRIOR PLING DATE: 2000-10-31
## PRIOR PLING DATE: 2000-10-31
## PRIOR PLING DATE: 2000-10-31
## SOFTWARE: PATEURING DATE: 2001-07-16
## NUMBER OF SEQ ID NOS: 94
## SOFTWARE: PATEURING DATE: 2001-07-16
## SOFTWARE: PATEUR
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Sequence 69, Application US/10369405

Publication No. US20030224400A1

GENERAL INFORMATION:

TITLE OF INVENTION: THEREOF

PRIOR APPLICATION NUMBER: U.S. 60/249,613

PRIOR FILING DATE: 2000-11-17

PRIOR PELING DATE: 2000-12-21

PRIOR FILING DATE: 2000-12-21

PRIOR FILING DATE: 2000-12-21

PRIOR FILING DATE: 2000-10-16

PRIOR FILING DATE: 2010-07-16

NUMBER OF SEQ ID NOS: 94

SOFTWARE: PATENTING NOS: 94
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Best Local Similarity 100.
Matches 4; Conservative
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Matches 4; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                              NGTF 14
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   NGTF 36
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US-10-369-405-69
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US-10-369-405-42
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RESULT 19

33 NGTF 36

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TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, AND VARIANTS;

TITLE OF INVENTION: THEREOF;
FILE REFERENCE: D0075A CIP;
CURRENT PELLOR DATE: 2003-02-14

PRIOR APPLICATION NUMBER: U.S. 60/249,613

PRIOR APPLICATION NUMBER: U.S. 60/249,613

PRIOR APPLICATION NUMBER: U.S. 60/249,613

PRIOR PILING DATE: 2000-11-17

PRIOR APPLICATION NUMBER: U.S. 60/257,611

PRIOR PILING DATE: 2000-12-21

PRIOR PILING DATE: 2000-12-21

PRIOR PILING DATE: 2000-12-21

PRIOR PILING DATE: 2001-07-16

NUMBER OF SEQ ID NOS: 94

SOFTWARE: PatentIn version 3.2

SEQ ID NO 72

LENGTH: 15
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GENERALI INFORMATION:

APPLICANT: BERISEETER, RENEE

APPLICANT: BERISEETER, RENEE

APPLICANT: BERNING, JAKOB

APPLICANT: BERNING, JAKOB

APPLICANT: SCHERAEL, SOREN

APPLICANT: SCHERAEL, SOREN

APPLICANT: GOLDSTEIN, NEIL I.

APPLICANT: HANSEN, PER HERTZ

TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS

FILE REPRENEUE: 1874-4051018

FULN REPRENEUE: 1874-4051018

CURRENT FILING DATE: 2001-09-24

PRIOR APPLICATION NUMBER: 09/146,127

PRIOR APPLICATION NUMBER: 09/146,127

PRIOR APPLICATION NUMBER: 09/146,127

SOFTWARE: PARCHIN VOIC 2.227

SEQ ID NO 606

TENGTH: 18

TYPE: PRI
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US-09-962-756-606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 15;
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; Sequence 606, Application US/09962756
; Publication No. US20030195147A1
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Best Local Similarity 100.
Matches 4; Conservative
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Matches 4; Conserv
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                          gequence 2046, Application US/10225567A

publication No. US20030113798A1

GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Burmer, Glenna C.
APPLICANT: Burmer, Glenna C.
APPLICANT: Burmer, Glenna C.
APPLICANT: Rough, Christine L.
TILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT APPLICATION NUMBER: 60/257,144
PRIOR PLING DATE: 2000-12-19
PRIOR PLING DATE: 2000-12-19
PRIOR PLING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTHARE: Patentin version 3.1
SEQ ID NO 2046
LENGTH: 15
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publication No. US20030224400A1

GENERAL INDORMATION:
TITLE OF INVENTION: WOUEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPREMY11, AND VARIANTS
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION NUMBER: U.S. 60/249,613
PRIOR PAPLICATION NUMBER: U.S. 60/249,613
PRIOR PAPLICATION NUMBER: U.S. 60/257,611
PRIOR APPLICATION NUMBER: U.S. 60/305,818
PRIOR PILING DATE: 2000-12-21
PRIOR PAPLICATION NUMBER: U.S. 60/305,818
PRIOR FILING DATE: 2001-07-16
NUMBER OF SEQ ID NOS: 94
SOFTWARE: PRECENT NOS: 94
SEQ ID 
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Pred. No. 2.1e+02;
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Sequence 72, Application US/10369405

Publication No. US20030224400A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company
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100.0%; Pre
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Best Local Similarity 100.
Matches 4; Conservative
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ORGANISM: Homo sapiens
US-10-225-567A-2046
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Best Local Similarity
Matches 4; Conserv
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US-10-369-405-60
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US-10-369-405-60
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US-10-253-286-312

US-10-253-286-312

Sequence 312, Application US/10253286

Publication No. US20040058881A1

GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU, MINZHEN
TITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
TILE REFERENCE: REH-2015
CURRENT APPLICATION NUMBER: US/10/253,286
CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR PLING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 905
SEQ ID NO 312
SEQ ID NO 312
TYPE: DETAILS THE TENTOR DATE: 2015-01-17
TYPE: DETAIL TENTOR DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 905
THE OFFICIAL OFFICE TENTOR DATE: 2015-01-17
TYPE: DETAIL OFFICE TENTOR DATE: 2015-01-17
TYPE: DETAIL OFFICE TENTOR DATE: 2015-01-17
TYPE: DETAIL OFFICE TENTOR DATE: 2015-01-14
TYPE: DETAIL OFFIC
Sequence 312, Application US/10245871

Publication No. US20030235594A1

GENERAL INFORMATION:

APPLICANT: HUMPHREYS, ROBERT

APPLICANT: HUMPHREYS, ROBERT

TITLE OF INVENTION: I1-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES

FILE REFERENCE: REH-2013

CURRENT APPLICATION NUMBER: 10/197,000

PRIOR FILING DATE: 2003-01-09

PRIOR PLICATION NUMBER: 10/197,000

PRIOR PLICATION NUMBER: 10/197,000

PRIOR PLILING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 905

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: I1-key/MHC Class II/MHC Class I CEA hybrid OTHER INFORMATION: peptide
FERATURE:
NAME/KEY:
NAME/KEY:
NAME/KEY:
OTHER INFORMATION: a-aminovaleric acid
FEATURE:
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FEATURE:
NAME/KEY: NOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 23.5%; Score 23; DB 15; 18est Local Similarity 100.0%; Pred. No. 3.3e+02; Matches 4; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: C-term amidated US-10-245-871-312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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       US-10-253-471-606

| Sequence 606, Application US/10253471 |
| Sequence 606, Application US/10253471 |
| Publication No. US2000236190A1 |
| GENERAL INFORMATION: |
| APPLICANT: PILLUTLA, RENUKA et al. |
| TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS |
| FILE REFERENCE: 1878-4057 |
| CURRENT APPLICATION NUMBER: US/10/253,471 |
| PRIOR PILING DATE: 2002-09-24 |
| PRIOR PILING DATE: 2000-03-29 |
| PRIOR FILING DATE: 2000-03-29 |
| PRIOR FILING DATE: 1998-09-02 |
| PRIOR FILING DATE: 1998-09-02 |
| NUMBER OF SEQ ID NOS: 2227 |
| SOFTWARE: Patentin Ver. 2.1 |
| SEQ ID NO 606 |
| LENGTH: 18
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Fublication No. US20040023887A1

GENERAL INFORMATION:

TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS

FILE REPERENCE: 18784056

CURRENT APPLICATION NUMBER: US/10/253,493

CURRENT FILING DATE: 2002-09-24

PRIOR APPLICATION NUMBER: 09/562,756

PRIOR FILING DATE: 2001-09-24

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1988-09-02

NUMBER OF SEQ ID NOS: 2227

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 606

LENGTH: 18
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US-10-253-471-606
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US-10-253-493-606
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100.0%; Pred. No. 2.5e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 4; Conservative
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Matches 4; Conserva
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US-10-253-286-312

RESULT 25 US-10-245-871-312

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Length 24; 0; Indels

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Sequence 168021, Application US/10424599

| Publication No. US2040031072A1
| Publication No. US2040031072A1
| Publication No. US2040031072A1
| APPLICANT: La Rosa Thomas J
| APPLICANT: La Royalic David K
| APPLICANT: Zhou Yihua
| APPLICANT: Cao Yongwai
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Show Yihua
APPLICANT: Zhow Yihua
APPLICANT: Car Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 30
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US-10-424-599-168021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT3847_108700C.1.pep
US-10-424-599-152465
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; Sequence 152465, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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US-09-209-799D-22
; Sequence 22, Application US/09209799D
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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ORGANISM: Glycine max
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 NGTF 36
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| APPLICANT: Zimmerman, Daniel S |
| TITLE OF INTENTION: TELL BINDING LIGAND PEPTIDES, PEPTIDE |
| FILE REFERENCE: CS-112 |
| FILE REFERENCE: CS-112 |
| FILE REFERENCE: Z002-11-22 |
| PRIOR APPLICATION NUMBER: US/10/296,317 |
| PRIOR APPLICATION NUMBER: US/10/206548 |
| PRIOR APPLICATION NUMBER: PCT/US07/16793 |
| PRIOR FILING DATE: 2001-05-24 |
| PRIOR FILING DATE: 2001-05-24 |
| PRIOR FILING DATE: 2001-05-24 |
| SOGTWARE: Patentin version 3.1 |
| SEQ ID NO 67 |
| LENGTH: 26 |
| LENGTH: 27 |

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Publication No. US20040057968A1
| FURLICAUT: CLICANT. CORP.
| APPLICANT: Zimmerman, Daniel S
| TITLE OF INVENTION: T CELL BINDING LIGAND PEPTIDES, PETIDE FILE REFERENCE: CS-112
| CURRENT PAPLICATION NUMBER: US/10/296,317
| CURRENT FILING DATE: 2002-11-22
| PRIOR APPLICATION NUMBER: DCT/US07/16793
| PRIOR FILING DATE: 2001-05-24
| NUMBER OF SEQ ID NOS: 96
| SOFTWARE: PatentIn Version 3.1
| SEQ ID NO 59
| LENGTH: 28
        23.5%; Score 23; DB 15; Length 24; 100.0%; Pred. No. 3.3e+02; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  i OTHER INFORMATION: Peptide construct
US-10-296-317-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 67, Application US/10296317; Publication No. US20040057968A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                 Conservative
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Matches 4; Conserv
Query Match
Best Local Similarity
Matches 4; Conserv
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NGTF 26
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US-10-296-317-59
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NUMBER OF SEQ ID NOS: 115
SOFTWARE: Patentin version 3.1
SEQ ID NO 113
LENGTH: 37
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APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
                                                                                                                                                                  Query Match 23.5
Best Local Similarity 100.
Matches 4; Conservative
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Sun, Yongming
Liu, Chenghua
Chen, Sei-Yu
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ORGANISM: Homo sapien
US-09-995-494-113
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Best Local Similarity
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APPLICANT:
APPLICANT:
SEQ ID NO 5
LENGTH: 31
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APPLICANT: Garman, Jonathan David
APPLICANT: Garman, Jonathan David
APPLICANT: Candia III, Albert Frederick
APPLICANT: Arbor Vita Corporation
TITLE OF INVENTION: CLASP-5 Transmembrane Protein
FILE REFERENCE: 020054-000511US
CURRENT APPLICATION NUMBER: US/09/736,960
PRIOR APPLICATION NUMBER: US 60/160,860
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 60/170,453
PRIOR PLING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 60/176,195
PRIOR APPLICATION NUMBER: US 60/176,195
PRIOR PILING DATE: 2000-01-14
PRIOR PLING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: US 60/182,296
PRIOR PRING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: US 60/182,296
PRIOR PLING DATE: 2000-02-14
                                        APPLICANT: Hermeling, Ronald
APPLICANT: Hoffmann, James
APPLICANT: Hoffmann, Chakravarthy
TITLE OF INVENTION: GLUCAGON-LIKE PEPTIDE-1 CRYSTALS
FILE REFERENCE: X-10242
                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/209,799D CURRENT FILING DATE: 1998-12-11 NUMBER OF SEQ ID NOS: 29 SOFTWARE: Patentin version 3.0 SEQ ID NO 22 LENGTH: 31
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PRIOR APPLICATION NUMBER: US 60/176,195
PRIOR APPLICATION NUMBER: US 60/176,195
PRIOR APPLICATION NUMBER: US 60/182,296
PRIOR PILING DATE: 2000-01-14
PRIOR PELING DATE: 2000-02-14
PRIOR PELING DATE: 2000-04-11
PRIOR PELING DATE: 2000-10-13
PRIOR PELING DATE: 2000-10-13
PRIOR PELING DATE: 2000-10-13
PRIOR PELING DATE: 2000-10-13
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APPLICATION NUMBER: US 60/240,543
FILING DATE: 2000-10-13
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Patent No. US20020102267Al
GENERAL INFORMATION:
APPLICANT: Lu, Peter
Publication No. US20010014666A1
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SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Artificial
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Best Local Similarity
Matches 4; Congerv
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APPLICANT: Chem, Sei-Yu
TITLE OP INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
FILE REFERENCE: DEX-0293
CURRENT APPLICATION NUMBER: US/09/995,494
FRIOR APPLICATION NUMBER: 60/253,176
PRIOR APPLICATION NUMBER: 60/253,176
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                                                                                                                 Length 31;
                                                                                                                                                              Indels
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Publication No. US20030045464A1

GENERAL INFORMATION:
APPLICANT: Hermeling, Ronald
APPLICANT: Narasimhan, Chakravarthy
TITLE OF INVENTION: GLUCAGON-LIKE PEPTIDE-1 CRYSTALS
FILE REPERBUCE: X-10242
CURRENT APPLICATION NUMBER: US/09/997,792
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.0
                                                                                                                 23.5%; Score 23; DB 9; Le
100.0%; Pred. No. 4.2e+02;
tive 0; Mismatches 0;
TYPE: PRT ORGANISM: Homo sapiens OCGANISM: Homo sapiens US-09-736-960-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: synthetic construct US-09-997-792-22
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TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 100.(
Matches 4; Conservative
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SEQ ID NO 1419
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APPLICANT: Guthrie, K.
APPLICANT: Guthrie, K.
APPLICANT: Ansert, M.
APPLICANT: Ansert, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYDEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
TITLE OF INVENTION: PROPERTIES
TITLE OF INVENTION: PROPERTIES
TITLE OF INVENTION NUMBER: US/10/351,641
CURRENT APPLICATION NUMBER: US/250,641
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 1757
SOOTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1420
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Publication No. US200301868741

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Guthrie, K.

APPLICANT: Merutka, G.

APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

TITLE OF INVENTION: HYBRE: US/10/351,641

CURRENT APPLICATION NUMBER: US/10/351,641

CURRENT PILING DATE: 2003-01-24

PRIOR APPLICATION NUMBER: 09/350,641

PRIOR PAPLICATION NUMBER: 09/350,641

PRIOR APPLICATION NUMBER: 09/350,641

PRIOR PILING DATE: 1999-05-20

PRIOR FILING DATE: 1999-05-20
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                       Length 37;
                                                                       0; Indels
                       DB 9;
     23.5%; Scc. 100.0%; Pred. No. sc. ... 0; Mismatches
                                                                                                                                                                                                                                                                  US-10-351-641-1420
; Sequence 1420, Application US/10351641
; Publication No. US20030186874A1
; APPLICANT: Barney, S.
APPLICANT: Cuthrie, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Core polypeptide US-10-351-641-1420
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
                    Query Match 23.5
Best Local Similarity 100.
Matches 4; Conservative
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## APPLICANT: Barner, M.
## APPLICANT: Lambert, D.
## APPLICANT: NUMBER: US/10/351,641
## PRIOR APPLICATION NUMBER: US/350,641
## PRIOR PILING DATE: 1999-07-09
## PRIOR PILING DATE: 1999-07-09
## PRIOR PILING DATE: 1999-05-20
## PRIOR PILING DATE: 1998-05-20
## PRIOR PILING DATE: 1999-05-20
## PILING DATE: 
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APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Guthrie, K.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
APPLICANT: Lambert, D.
APPLICANT: Lambert, D.
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
PRIOR APPLICATION NUMBER: 09/350,641
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100.0%; Pred. No. 5.3e+02;
tive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0;
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; Publication No. US20030186874A1
; GENERAL INFORMATION:
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Publication No. US20030186874A1
GENERAL INFORMATION:
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-10-351-641-1419
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APPLICANT: Guthrie, K.
APPLICANT: Anwer, G.
APPLICANT: Anwer, D.
APPLICANT: Anwer, D.
APPLICANT: Lamber, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR PLING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
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Pred. No. 5.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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                                                                                                                                                                                                                                                                                                                                             23.5%; Score 23; DB 14; 100.0%; Pred. No. 5.4e+02; tive 0; Mismatches 0;
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CCATION: 4, 8

OTHER INFORMATION: Xaa = Abu (aminobutyric acid)
US-10-351-641-1748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.5%; bcc.
100.0%; Pred. No. _
0; Mismatches
FRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1748, Application US/10351641; Publication No. US20030186874A1; APPLICANT: Barney, S. APPLICANT: Guthrie, K.
                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Core polypeptide US-10-351-641-1747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Core polypeptide
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; Patent No. US20020160491A1
; GENERAL INFORMATION:
                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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US-09-912-628-9
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TLE OF INVENTION: Human Serpin Polynucleotides, Polypeptides, and Antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (32)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (33)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-912-628-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.5%; Score 23; DB 9; Le
100.0%; Pred. No. 5.6e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
               TILLE REFERENCE: PT001P2
CURRENT APPLICATION NUMBER: US/09/912,628
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: PCT/US01/02484
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/178,769
PRIOR APPLICATION NUMBER: E07/US00/05082
PRIOR APPLICATION NUMBER: PCT/US00/05082
PRIOR APPLICATION NUMBER: PCT/US00/05082
PRIOR PILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 9
LENGTH: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: February 24, 2005, 15:42:01 Job time : 83.0406 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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5.1.6	Compugen
version	- 2005
GenCore	(c) 1993
	Copyright

- protein search, using sw model OM protein Run on:

February 24, 2005, 15:12:40; Search time 21.8537 Seconds (without alignments) 246.555 Million cell updates/sec

Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_79:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	cription	probable ABC trans	probable secreted	130K paracrystalli	paracrystalline su	S-layer protein Rs	prepilin [imported	transferrin-bindin	hypothetical prote	Rhs element associ	급	me c	를	alpha-1-acid glyco	ğ	colicin V precurso	Ig upsilon chain -	급		rote	probable membrane	hypothetical prote	ŭ	yijD protein - Esc	hypothetical prote		,-	B. subtilis YhdG p	probable gntR-fami	hypothetical prote
SUMMARIES	ID	D70986	T34986	84	A48995	C87374	AG1028	D81832	E81911	E85731	D96953	T40973	A96525	B26300	A82829	B82829	S43147	E69223	AD3596	844709	AD0935	D86088	G91240	G65203	S21565	E97103	AD1123	AF1483	T36750	D64339
	DB	!			~																									
	Length	865	220	312	1026	1073	435	698	42	49	57	83	84	102	102	102	110	111	112	116	119	119	119	. 119	120	121	123	132	134	135
o je	Query Match		•		25.5							•				•			•	23.5		٠	•	•		•			•	
	Score	28	25	25	25	25	24	24	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23
	Result No.	1	~	m	4	S	9	7	æ	σ	10	11	12	13	14	15	16		18	19	20	21	22	23	24	25	26	27	28	29

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A99362 T24916 S67149 T49689	G91103 E71041 B85949 T33494 S72492	A69883 F69744 T21761 T02166	A32795 H97061 T07597
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138 138 141 143	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	147 151 152 156	156 157 158
23.5 23.5 23.5 23.5	23.5 23.5 23.5 53.5 53.5	23.5 23.5 23.5	23.5 23.5
3333	73 3 3 3 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	33333 53333	23 23 23
33 33 33 33 33	w w w w w 4 w o t w	6 4 4 0 1 4	4 4 4 4 4 5 5 4 5

ALIGNMENTS

_	RESULT 1
	D70986
	probable ABC transporter Rv1747 - Mycobacterium tuberculosis (strain H37RV)
	C;Species: Mycobacterium tuberculosis
	C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
	C;Accession: D70986
_	R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
	; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
	Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
_	Nature 191 517-544 1998

Nature 393, 537-544, 1998
Aptubrors: Sqarea, R; Sulaton, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Authors: Sqarea, R; Sulaton, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID:98295987; PMID:9634230
A; Accession: D70986
A; Accession: D70986
A; Accession: D70986
A; Croser-references: UNIPROT:065934; GB:Z95890; GB:AL123456; NID:g3242245; PIDN:CAB09333.
A; Residues: 1-865 cCOL
A; Experimental source: strain H37Rv
C; Genetics:
A; Experimental source: strain H37Rv
C; Genetics:
A; Gene: Rx1147
C; Genetics: A; Affene: Rx1147; ATP-binding c
C; Superfamily: Mycobacterium tuberculosis probable ABC transporter Rv1747; ATP-binding c
C; Keywords: ATP
F; 335-528/Domain: ATP-binding cassette homology cABC>

Gaps .. 0 Query Match 28.6%; Score 28; DB 1; Length 865; Best Local Similarity 29.2%; Pred. No. 70; Matches 7; Conservative 0; Mismatches 17; Indels

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270 NGTFVNGARVDAALLHDGDVVTIG 293 33 NGTFXXXXXXXXXXXG 56 ద ò

RESULT 2

probable secreted protein - Streptomyces coelicolor

Cipcaeis: Streptomyces coelicolor

Cipcaeis: Streptomyces coelicolor

Cipcaeis: Streptomyces coelicolor

Cipcaeis: Os-Nov-1999 #text_change 09-Jul-2004

Cipcaesion: T34986

R;Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, August 1998

A;Reference number: Z21550

A;Reference number: Z1550

A;Reference number: Z1550

A;Reference number: Z1550

A;Reference: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-220 <OLL>
A;Cross-references: UNIPROT: O86667; EMBL: AL031182; PIDN: CAA20163.1; GSPDB: GN00070; SCOED

A;Experimental source: strain A3(2)

A, Gene: SCOEDB:SC4A2.11c C,Genetics:

25

Fri Feb

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314 NDTFVAGEVAGAATLTVGDTLSGG 337
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Best Local Similarity 25.0%;
Matches 6; Conservative (
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Matches 6; Conservative (
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Similarity 25.0%;
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A;Molecule type: DNA
A;Residues: 1-698 <PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
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        A; Accession: C87374
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A48895
paracystalline surface layer protein RsaA - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Dete: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A48995
R;Gilchrist, A.; Fisher, J.A.; Smit, J.
Can. J. Microbiol. 38, 193-202, 1992
A;Title: Nucleocitde sequence analysis of the gene encoding the Caulobacter crescentus pa
A;Title: Nucleocitde sequence analysis of the gene encoding the Caulobacter crescentus pa
A;Accession: A48995
A;Accession: A48995
A;Residues: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-1026 cdIL>
A;Residues: 1-1026 cdIL>
A;Residues: 1-1026 cdIL>
A;Residues: 1-1026 cdIL>
A;Residues: acquence inconsistent with the nucleotide translation
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:116173, NCBIP:116174)
                                                                                                                                                                                                                                                           A31846

130K paracrystalline protein - Caulobacter crescentus (fragment)

C;Species Caulobacter crescentus

C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 20-Mar-1998

C;Accession: A31846

R;Fisher, J.A.; Smit, J.; Agabian, N.

A;Title: Transcriptional analysis of the major surface array gene of Caulobacter crescental A;Reference number: A31846; MUID:89008089; PMID:3049545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-layer protein RsaA [imported] - Caulobacter crescentus
S-layer protein RsaA [imported] - Caulobacter crescentus
C;Species Caulobacter crescentus
C;Species 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: C87374
S;Nierman, W.C.; Peldblyum, T.V.; Paulosn, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, B.; Laub, M.T.; DeBby, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 25; DB 2; Length 312;
Pred. No. 1.5e+02;
0; Mismatches 18; Indels
25.5%; Score 25; DB 2; Length 220; 26.3%; Pred. No. 16+02; tive 1; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-312 <FIS>
A;Cross-references: GB:M22663; NID:g556033; PID:g556034
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25.0%;
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
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RiParkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 201.
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serove A;Reference number: AB0502; MUID:21534947; PMID:11677608
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**Rarkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell]

**Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

**A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.

**A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.

**A;Reference number: A81775; MUID:20222556; PMID:10761919
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A,Experimental source: gerogroup A, strain Z2491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepilin [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1073 <STO>
A;Cross-references: GB:AE005673; NID:g13422297; PIDN:AAK22991.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC1007
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A;Cross-references: GB:AL513382; PIDN:CAD09328.1; PID:g16505328; GSPDB:GN00176
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Pred. No. 5.8e+02;
0; Mismatches 18; Indels
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                                                                                                                                                                                                                                                                  Score 25; DB 2; 1
Pred. No. 4.9e+02;
0; Mismatches 18;
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Pred. No. 3.6e+02;
0; Mismatches 18
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A, Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo A, Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-57 < KUR>
A;Cross-treferences: UNIPROT:Q97LW9; GB:AE001437; PIDN:AAK78415.1; PID:g15023290; GSPDB:G
A;Experimental source: Clostridium acetobutyllcum ATCC824
C;Genetics:
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*Residues 1.83 -LYN>
A;Cross-references: UNIRROT:094581; EMBL:AL031966; PIDN:CAA21442.1; GSPDB:GN00068; SPDB:
A;Experimental source: strain 972h-; cosmid c1442
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Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Liuros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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C; Genetics:
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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C;Accession: T40973

Sibyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G. submitted to the EMBL Data Library, October 1998
A;Reference number: 221961
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A;Introns: 29/1; 65/1
C;Superfamily: mammalian cytochrome-c oxidase chain VIb
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Pred. No. 1.3e+02;
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A,Status: preliminary; translated from GB/EMBL/DDBJ
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100.0%; Pred. No. 89;
ive 0; Mismatches
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
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A;Molecule type: DNA
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                                                                 A;Accession: D96953
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hypothetical protein NWA1420 [imported] - Neisseria meningitidis (strain Z2491 serogroup Cispeciaes Neisseria maningitidis
C;Speciaes Neisseria maningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: B81911

R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel R;Parkhill, J.; Adgels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Mature 404, 502-506, 2000

A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUD:20222556; PMID:10761919
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D96953
Dypothetical protein CAC0435 [imported] - Clostridium acetobutylicum
C,Species: Clostridium acetobutylicum
C,Species: Clostridium acetobutylicum
C,Bate: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C,Accession: D96953
R,Nolling, J., Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q9JUA3; GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB8466
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
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Rhs element associated protein Z2255 [imported] - Escherichia coli (strain O157:H7, subs
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85731
C;Accession: B85731
Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
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A,Experimental source: strain O157:H7, substrain EDL933
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100.0%; Pred. No. 66;
.ive 0; Mismatches 0; Indele
                                                                                     590 NGTLTADNROAATFTIVGDIEGNG 613
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                                      33 NGTFXXXXXXXXXXXGDXXXXG
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-49 <STO>
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Sawasak
Silveira
A.L.; Za
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C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82829
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Feference number: A82515; MUID:20365717; PMID:10910347
A;Accession: B82829
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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; All

Briones, M.S.; Bueno, M.R.D.; Canargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohmel

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.D.; Krieger, J.E.; Kuramae, E.E.; Laigre

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.

R;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sal. R;Sirva, R.C.; Palmieri, D.A.

A;Authors: da Silva, A.C.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.M.; Silva Jr., W.A.; da Silveira,

A;Contents: annotation

C;Genetics:
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           Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Alathores da Silva, A.C.R.; da Silva, A.G. R.; Silva Jr., W.A.; da M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A;Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                        ö
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CiSpecies: Anas platyrhynchos (domestic duck)
CiSpecies: Anas platyrhynchos (domestic duck)
CiDate. 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 11-Jan-2000
CiAccession: S41147
Rimagor, K.B.; Higgins, D.A.; Middleton, D.L.; Warr, G.W.
Rimagor, K.B.; Higgins, D.A.; Middleton, D.L.; Warr, G.W.
A; Reference number: S43145
A; Reference number: S43147
A; Status: preliminary
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                  Length 102;
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                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                              23.5%; Score 23; DB 2; Le ilarity 100.0%; Pred. No. 1.6e+02; Conservative 0; Mismatches 0;
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Best Local Similarity
Matches 4; Conserv
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Matches 4; Conser
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A;Molecule type: DNA
A;Residues: 1-102 <SIM>
                                                                                                                                                      A;Contents: annotation C;Genetics: A;Gene: XF0262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 NGTF 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97
                                                                                                                                                                                                                                                                                                  Query Match
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A82829
collicin V precursor XF0262 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Accession: A82829
Collicin A82829
C;Accession: A82829
A;Accession: A82829
A;Accessi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-102 <CCO>
A;Cross-references: UNIPROT:Q91X23
A;Cross-references: UNIPROT:Q91X23
C;Comment: At least 2 genes coding for different forms of alpha-1-AGP appear to be prese
C;Comment: Alpha-1-AGP is synthesized in the liver, the synthesis being controlled by g1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nighternate names: orosomucoid
C;Species: Mus musculus (house mouse)
C;Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 09-Jul-2004
C;Datession: B26300
R;Cooper, R.; Papaconstantinou, J.
J. Biol. Chem. 261, 1849-1853, 1986
A;Title: Evidence for the existence of multiple alpha-1-acid glycoprotein genes in the A;Reference number: A26300; MUID:86111861; PMID:3003086
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C; Supwords: acute phase; glycoprotein; liver; plasma
F;1-101/Domain: lipocalin homology (fragment) <LIP>
F;8-101/Disulfide bonds: #starus predicted
F;8-10, Zi/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                 Length 84;
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                                                                                                              23.5%; Score 23; DB 2; L6
100.0%; Pred. No. 1.3e+02;
ive 0; Mismatches 0;
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                                                                             Query Match
Best Local Similarity 100.
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A; Map position: 1
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opacity protein opaB - Neisseria meningitidis (isolate 21213) (fragment)
C;Species: Neisseria meningitidis
A;Variety; isolate 21213
C;Date: 13-Jan-1995 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: 844709
C;Accession: 844709
Mol. Microbiol. 12, 171-180, 1994
A;Title: Microevolution within a clonal population of pathogenic bacteria: recombination A;Reference number: 844705; MUID:94335637; PMID:7520117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:051089; EMBL:U03409; NID:g432174; PIDN:AAA61550.1; PID:g4321 A;Experimental source: isolate Z1213; strain serogroup A; clone pFLOB2510 A;Note: expression of opacity proteins is regulated by the number of translated repeat e of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cjaccession: AD0935
R; Parkhil, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica servo, A;Reference number: AB0502; MUID:21534947; PMID:11677608
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hypothetical protein yijD [imported] - Escherichia coli (strain O157:H7, substrain EDL93
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(Superfamily: opacity protein
C;Superfamily: opacity protein
C;Keywords: cell surface component; transmembrane protein
F;1-37/Domain: extracellular #status predicted <EXT2>
F;7-22/Region: hypervariable region HVI
F;38-52/Domain: transmembrane #status predicted <TM4>
F;61-71/Domain: transmembrane #status predicted <TM4>
F;77-116/Region: hypervariable region HV2
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1.8e+02;
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypotheeical protein MTH922 - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium
C;Species: Methanobacterium
C;Bate: O5-Dec-1997 #sequence Tevision O5-Dec-1997 #text_change O9-Jul-2004
C;Accession: E6923
K;Smith, D.R.; Doucette-Stamm, L.A.; Deluughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
K;Smith, D.; Spadafora, R.; Vicaire, R.; Wano, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
K; S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: E6923
A;Accession: E6923
A;Accession: E6923
A;Accession: E6923
A;Accession: E69223
A;A
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C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AD3596
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
B; Mazur, M.; Goltsman, B.; Selkov, B.; Blzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Status: preliminary
A;Molecule type: DNA
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A;Experimental source: strain 16M
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hypothetical cytogolic protein BMEI10693 [imported] - Brucella melitensis (strain 16M)
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                                       A;Cross-references: EMBL:X78355; NID:g468612; PID:g468613
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                            23.5%; Score 23; DB 2; Length 110; 100.0%; Pred. No. 1.7e+02; tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.7e+02;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
A; Residues: 1-110 <MAG>
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A;Start codon: TTG
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A,Map position: II
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Query Match 23.5%; Score 23; DB Best Local Similarity 100.0%; Pred. No. 1.6 Matches 4; Conservative 0; Mismatches
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Best Local Similarity 100.0
Matches 4; Conservative
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A;Accession: $21565
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Best Local Similarity
Matches 4; Conserv
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        A;Gene: yijD
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E97103
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4991240

hypothetical protein EC64895 [imported] - Escherichia coli (strain O157:H7, substrain RI
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Bscherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: 691240
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
A;Tele: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gench A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Status: poesiminary
A;Molecule type: DNA
A;Residuse: 1-119 etAty
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G65203

yij) protein - Escherichia coli (strain K-12)

C;Species: Eacherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

C;Accession: G65203

R;Blattner, P.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc.
A;Reference 277, 1453-1462, 1997

A;Reference number: A64720; MUD:97426617; PMID:9278503

A;Reference number: A64720; MUD:97426617; PMID:9278503

A;Accession: G65203

A;Accession: G65203

A;Actus: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-119 <-BLAT>
A;Coss-references: UNIPROT:P27308; GB:AE000470; GB:U00096; NID:g2367332; PIDN:AAC76946.
                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-119 <STO.
A;Cross-references: UNIPROT:P27308; GB:AE005174; NID:g12518891; PIDN:AAG59168.1; GSPDB:G
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
A;Gene: yijD
C;Species: Bscherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: D; Bunket
B;Perna, N.T.; Plunket
III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A88480; MUID:21074935; PMID:11206551
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
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Best Local Similarity
Matches 4, Conserva
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C; Species: Clostridium acetobutylicum
C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C; Accession: E97103
C; Accession: E97103
R; Nolling, J: Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J: Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
Bacteriol. 183, 4823-4838, 2001
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos
A; Reference number: A96900; MUID:21359325; PMID:21359325
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A;Experimental source: Clostridium acetobutylicum ATCC824
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD1123
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H., D.; Jones, L.M.; Karst, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P27308; EMBL:X66026; NID:943236; PIDN:CAA46824.1; PID:943239
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C;Species: Escherichia coli
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S21565
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       Length 119;
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100.0%; Pred. No. 1.8e+02;
ive 0; Mismatches 0; Indels
DB 2; Le
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A; Gene: SCOEDB:SCI11.17c
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C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Datession: AFIGURATION OF PROBLEM OF P.; Bloecker
C;Dataser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
S;Glaser, P.; Frangeul, L.; Buchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
A;Authors: Kreft, J; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AF1483
A;Status: preliminary
A;Molecule type: DNA
A; Carlos A;Accession: AF1483
A;Status: Dreliminary
A;Molecule type: DNA
Science 294, 849-852, 2001

Ajauthors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Title: Comparative genomics of Listeria species.

A; Reference number: AB1077; MUID:21537279; PMID:11679669

A; Accession: AD1123

A; Accession: AD1123

A; Molecule preliminary

A; Molecule: Draiminary

A; Residues: 1-123 cGLA

A; Residu
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A;Cross-references: UNIPROT:Q92EQ3; GB:AL592022; PIDN:CAC95638.1; PID:g16412834; GSPDB:G
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A;Gene: 1mo0387
C;Superfamily: Bacillus subtilis hypothetical protein ydhG
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Best Local Similarity 100....
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Best Local Similarity
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Cjaccession: D64339
RjBult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.Bult, C.J.; White, O.; Ousen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.I.; Overbeek, R.; Kirkess, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; reich, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64300; MUID:96337999; PMID:8688087
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A Molecule type: DNA
A; Residues: 1-138 «KULR»
A; Cross-references: UNIPROT: Q97WZ9; GB: AEO06641; NID: g13815234; PIDN: AAK42152.1; GSPDB: G
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C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 2-4 May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: A99362
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, Sarrett, Ra.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
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C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
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     Length 134;
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     DB 2; Le
2.1e+02;
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llarity 100.0%; Pred. No. 2.1e+02;
Conservative 0; Mismatches 0;
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C;Superfamily: conserved hypothetical protein MJ0315
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     Score 23;
Pred. No.
23.5%;
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Query Match 23.5
Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
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NGTF 130

NGTF 36

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-143 <HAY>
A; Gene: NCSP: B23L21.20
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A.Gene: PH1621
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A,Residues: 1-141 «JAU»
A,Cross-references: UNIPROT:Q08687; EMBL:Z75160; NID:g1420570; PID:e252106; PID:g1420571
A,Experimental source: strain S288C
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T49689
T49689
Whyothetical protein B23L21.20 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
C;Accession: T49689
R;Accession: T49689
R;Accession: T49689
R;Accession: T49689
A;Reference number: Z2502
A;Reference number: Z2502
A;Reference number: Z2502
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-143 <SCH>
A;Residues: 1-143 <SCH>
A;Residues: 1-143 <SCH>
C;Accession: T498 <ACH>
C;Accession: T498 <ACH>
C;Accession: T498 <ACH
A;Residues: 1-143 <SCH>
C;Genetics: BAC clone B23L21; strain OR74A
                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q22499; EMBL:Z68880; PIDN:CAA93096.1; GSPDB:GN00022; CESP:T1
A;Experimental source: clone T14G10
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             hypothetical protein T14G10.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24916
R;Wild, A.
submitted to the EMBL Data Library, January 1996
A;Reference number: Z19954
A;Accession: T24916
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S67149

hypothetical protein YOR252w - yeast (Saccharomyces cerevisiae)

hypothetical protein YOR252w - yeast (Saccharomyces cerevisiae)

NyAlternate names: hypothetical protein 05310

C;Species: Saccharomyces cerevisiae

C;Date: 12-011-1996 #sequence_revision 12-011-1996 #text_change 09-Jul-2004

C;Accession: S67149

R;Jauniaux, J.C.; Poirey, R.

submitted to the Protein Sequence Database, July 1996

A;Reference number: S67143

A;References with the protein Sequence Database, July 1996
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A,Cross-references: SGD:S0005778
A,Map position: 15R
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                 1-138 <WIL>
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A;Map position: 4
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hypothetical protein EC83799 [imported] - Escherichia coli (strain 0157:H7, substrain RIN
C,Species: Escherichia coli
C,Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: G91103

C;Accession: G91103

Askino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G., Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001

DNA Res. 8, 11-22, 2001

A;Fille: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q8XD02; GB:BA000007; PIDN:BAB37222.1; PID:g13363271; GSPDB:GN-k3;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
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A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
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A;Molecule type: DNA
A;Residues: 1-143 <KAW>
                                                                                                                                                                                                                                           Gaps
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A;Map position: 6
A;Introns: 67/3; 80/2
C;Superfamily: Neurospora crassa hypothetical protein B23L21.20
                                                                                                                                                   Query Match 23.5%; Score 23; DB 2; Length 143; Best Local Similarity 100.0%; Pred. No. 2.2e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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A,Residues: I-146 <BRA>
A,Cross-references: UNIPROT:Q7M222
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Matches 4; Conservative
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Best Local Similarity
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R,Brandstaedter, J.; Rossbach, C.; Theres, K.
R,Brandstaedter, J.; Rossbach, C.; Theres, K.
A)Ol. Gen. Genet. 252, 146-154, 1996
A;Title: Expression of genes for a defensin and a proteinase inhibitor in specific areas A;Reference number: S72491; MUID:96397493; PMID:8804387
A;Accession: S72492
          A;Cross-references: UNIPROT:Q8XD02; GB:AE005174; NID:912517463; PIDN:AAG58054.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-144 cGATA.
A;Cross-references: UNIPROT:Q9TZK4; EMBL:AF098987; PIDN:AAC67428.1; GSPDB:GN00020; CESP:A;Experimental source: strain Bristol N2; clone F40H3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Lycopersicon esculentum (tomato)
C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 09-Jul-2004
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A;Introns: 39/3; 72/1; 111/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F40H3.3
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                                                                                                                                                                                                                                                                                                                                                                                                   Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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Best Local Similarity 100..
---- 4; Conservative
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Matches 4; Conservative
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67 NGTF 70
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Circlession: A69883

Rikunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho A.; Bruich, S.D.; Erriston, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Kotter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueell, R.; M.; Rivolta, C.; Rocha, E.; Roche, M.; Sadaie, Y.; Saro, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tamamoto, H.; Vamane, K.; Vasumoto, V.; 
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R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho A.; Brlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

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N; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hibbert, H.; Holsappel, S.; Hollo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
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A;Experimental source: strain 168
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A;Accession: A69883
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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A; Experimental source: shoot, cv. Moneymaker
C; Superfandly: potato proteinase inhibitor PTI
C; Keywords: serine proteinase inhibitor
F;1-27/Domain: signal sequence #status predicted <SIG>
F;21-46/Product: probable proteinase inhibitor #status predicted <MAT>
F;33/Inhibitory site: Arg (trypsin) #status predicted
F;94/Inhibitory site: Arg (trypsin) #status predicted
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100.0%; Pred. No. 2.2e+02;
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A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueell Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, F.; Socifone, F.; Sekiguchi, J.; Sekowska, A.; Saronakeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Winters, P.; Winters, P.; Winters, P.; Winters, P.; Tosato, V.; Uchiyama, T.; Winters, P.; Winters, P.; Winters, P.; Tosato, V.; Uchiyama, A; Alttle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: A69580; MUID:98044033; PMID:9384377 translation not shown A; Molecule type: DNA A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-151 «KUN» A; Residues: 1-151 «KUN» A; Residues: 1-151 «KUN» A; Residues: 1-151 «KUN» A; Residues: 1-50 «Kuni 168 «C; Genetics: YbbK
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Best Local Similarity 100.
Matches 4; Conservative
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Search completed: February 24, 2005, 15:24:26 Job time : 27.8537 secs

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Q71sn5 helicobacter
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O9vmn1 caulobacter
Q7033 pichia fari
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Q8v7j9
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Copyright (c) 1993 - 2005 Compugen Ltd.
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                                      EMBL; AE000516; AAK46062.1; -.
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SEQUENCE 8
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STRAIN-CDC 1551 / Oshkosh;
STRAIN-CDC 1551 / Oshkosh;
BOI=10.1128/JB.184.19.5479-5490.2002;
DOI=10.1128/JB.184.19.5479-5490.2002;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen W.C., Gwinn M.L., Haft D.H., Hickey B.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M., Fraser C.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.

1. Sannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;

Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.

1. SIMILARITY: Balongs to the ABC transporter family.

EMBL; AE017239; ASSOGO16.1; -.

GO; GO:0005629; E:ATP binding; IEA.

GO; GO:0005624; E:ATP binding; IEA.

GO; GO:0000166; E:ATP as activity, coupled to transmembrane m.

GO; GO:0000166; E:Transport; IEA.
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                                                                                                 Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corymebacterineae; Mycobacteriaceae; Mycobacterium.
NCBL_TaxID=1770;
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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InterPro; IPRO03593; AAA ATPRSE.
InterPro; IPRO03593; AAA ATPRSE.
InterPro; IPRO03593; FHA.
InterPro; IPRO0055; FHA.
InterPro; IPRO00964; SMAD FHA.
Probom; Pro0006; ABC transporter; 1.
Probom; Pro0006; ABC transporter; 1.
SMART; SM00362; AAA; I.
SMART; SM00340; FHA; Z.
RROSITE; PS00211; ABC TRANSPORTER 1; 1.
RROSITE; PS00993; ABC TRANSPORTER 2; 1.
RROSITE; PS00906; FHA DOMAIN; 2.
RROSITE; PS00906; FHA DOMAIN; 2.
RROSITE; PS00906; FHA DOMAIN; 3.
ATP-binding; Complete Protecome; Hypothetical protein.
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. 1.7e+02;
...hes 17; Indels
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                                                  (TrEMBLrel. 27, Last sequence update) (TrEMBLrel. 27, Last annotation update)
               822 AA.
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                                                                                       OrderedLocusNames=MAP3466;
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Matches 7; Conservative
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               PRELIMINARY;
                                                                          Hypothetical protein.
                                                                                                                                                              SEQUENCE FROM N.A.
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                                     05-JUL-2004 (05-JUL-2004 (05-JUL-2004 (
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GO; GO:0016020; C:membrane; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.

GO; GO:0000166; F:nucleotide binding; IEA.

GO; GO:0006810; P:transport; IEA.
                                                                                                                                                GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:004226; F:ATPase activity, coupled to transmembrane m. . .; IEA.
GO; GO:000166; F:ATPase activity, coupled to transmembrane m. . .; IEA.
GO; GO:0006810; P:transport; IEA.
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
Harris D.B., Gordon S.V., Eighmeier K., Gas S., Barry C.E. III,
Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,
Connor R., Davies R.M., Devlin K., Fellwell T., Gentles S., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitchead S., Barrell B.G.,
Deciphering the biology of Mycobacterium tuberculosis from the
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 28.6%; Score 28; DB 2; Length 863 Local Similarity 29.2%; Pred. No. 3.2e+02; es 7; Conservative 0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUR.-2004 (TrEMBLrel. 26, Last annotation update)
PROBABLE CONSERVED TRANSMEMBRANE ATP-BINDING PROTEIN ABC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            863 AA; 91924 MW; 48CE63FDC73C2DA3 CRC64;
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Nature 393:537-544(1998).
-!- SIMILARITY: Belongs to the ABC transporter family.
EMBL, BX642577; CAB09333.1; -.
PIR; D70986; D70986.
J. Bacteriol. 184:5479-5490(2002).
-!- SIMILARITY: Belongs to the ABC transporter family.
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                                                                                                                                                                                                                                                                                                                                            Interpro; IPR003593; AAA ATPase.
Interpro; IPR003439; ABC_transporter.
Interpro; IPR000253; FHA.
Interpro; IPR009894; SMAD FHA.
Pfam; PF00005; ABC_tran; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom, PD000006; ABC transporter; 1.
SMART; SM00382; AAA; 1.
SMART; SM00240; FHA; 2.
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Li., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases

I. Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases

I. Submitted (SEP-2003) to the ABC transporter family.

EMBL; AR017239; AAS06615.1; -.

GO; GO:00016020; C:membrane; IEA.

GO; GO:0001624; F:ATP binding; IEA.

GO; GO:000166; F:ATPase activity; coupled to transmembrane m. ..; I

R GO; GO:000166; F:ATPase activity; Coupled to transmembrane m. ..; I

R GO; GO:000166; F:ATPase activity; Coupled to transmembrane m. ..; I

R GO; GO:000169; F:ATPase activity; FiA.

InterPro; IPR001439; AAA_ATPase.

InterPro; IPR001439; AAA_ATPase.

InterPro; IPR001439; ABC_transporter.

F Propo; PR00106; ABC_transporter;

R Propom; PR00106; ABC_transporter;

R Propom; PR00106; AAA; I.

R PRAMRT; SM001420; FHA, I.

R SMART; SM001420; FHA, I.

R SMART; SM001420; FHA, I.
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Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TAXID=1770;
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
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PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
PROSITE; PS50006; FHA_DOMAIN; 2.
ATP-binding; Complete proteomy
ATP-binding; Complete proteomy
SEQUENCE 873 AA; 93301 MW; 280DF91EA9B2B63F CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
OrderedLocusNames=MAP1457;
                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.6%; Score 28; DB 2; I
29.2%; Pred. No. 3.3e+02;
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                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=k10;
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                                                                                                   Q73UA3
Q73UA3;
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Matches
                                     RESULT 6
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A Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
A pryor M., Duthoy S., Garodin S., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
A Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
The complete genome sequence of Mycobacterium bovis.";
The complete genome sequence of Mycobacterium bovis.";
L. SIMILARITY: Belongs to the ABC transporter family.
BEMBL: BX2484478 11. -.
R GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016224; F:ATP binding: IEA.
GO; GO:0005224; F:ATP binding: IEA.
GO; GO:0006810; P:Ransport: IEA.
R GO; GO:0006810; P:Ransport: IEA.
R GO; GO:0006810; F:ATPARE activity, coupled to transmembrane m. .; IEA.
R GO; GO:0006810; F:ATPARE activity, coupled to transmembrane m. .; IEA.
R GO; GO:0006810; F:ATPARE C., Transporter.
R InterPro; IPR000353; FHA.
R InterPro; IPR000354; FHA.
R Pfam; PF00005; ABC trans; I.
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                        InterPro; IPRO00253; FHA.
InterPro; IPRO00894; SWAD FHA.
Pfam; PP00408; FHA.
Pfam; PP00408; FHA; 2.
ProDom; PD00006; ABC transporter; 1.
R SWART; SW00382; AAA; 1.
R SWART; SW00211; ABC_TRANSPORTER_1; 1.
R PROSITE; PS0093; ABC_TRANSPORTER_2; 1.
R PROSITE; PS0093; ABC_TRANSPORTER_2; 1.
R PROSITE; PS0000; FHA_DOMAIN; 2.
R PROSITE; PS0000; PAA; 92152 MW; 4997186C471E47E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 28.6%; Score 28; DB 2; Length 865; Local Similarity 29.2%; Pred. No. 3.3e+02; Pred. 7; Conservative 0; Mismatches 17; Indels
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
PROBABLE CONSERVED TRANSMEMBRANE ATP-BINDING PROTEIN ABC
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SEQUENCE 865 AA; 92152 MW; 4987186C471E47E8 CRC64;
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PROSITE; PS00211; ABC_TRANSPORTER 1; 1.
PROSITE; PS50093; ABC_TRANSPORTER_2; 1.
PROSITE; PS50006; FHA_DOMAIN; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270 NGTFVNGARVDAALLHDGDVVTIG 293
InterPro; IPR003439; ABC_transporter.
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Best Local Similarity 29.2.
T. Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium bovis.
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CSTRAIN=LSY54 / DSM 12343;

EXALUSELSY54 / DSM 12343;

EXALUSELSY54 / DSM 12343;

Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,

Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,

Teeling H., Leuechner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,

Klenk H.-P.;

The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium form permanently cold Arctic sediments.";

Environ. Microbiol. 6:887-902(2004).

EMBL, CR522870; CAG37299.1; -.

REL, CR522870; CAG37299.1; -.

REL, CR522870; CAG37299.1; -.

RINGEPRO; IPR000553; FHA.

REL, CR522870; CAG37299.1; -.

REL, CR522800, CAG4729.1; -.

REL, CR522800, CAG4729.1; -.

REL, CR522800, CAG47
                                                                                                                                                                                                                                                                                             MEDLINE-22225144; PubMed=12240834;

A Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,

A Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,

Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N.,

A Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

"Complete genome structure of the thermophilic cyanobacterium
Thermosynechococcus elongatus BP-1.";

Thermosynechococcus elongatus BP-1.";

EMBL; AP005373; BAC08787.1; -.

REMEL; AP005373; BAC08787.1; -.

RINEEPRO; IPR008984; SMAD_FHA.

R SMART; SW00240; FHA; 1.

R SMART; SW00240; FHA; 1.

R PROSITE; PS50006; FHA_DOMAIN; 1.

R COMplete proteome.

SEQUENCE 246 AA; 26355 MW; EAE4A94A64AD75C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Desulfotalea psychrophila.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
Desulfobulbaceae; Desulfotalea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 26.5%; Score 26; DB 2; Length 246; Best Local Similarity 29.2%; Pred. No. 3.2e+02; Matches 7; Conservative 0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.5%; Score 26; DB 2; Length 405; 31.6%; Pred. No. 5.1e+02; ive 0; Mismatches 13; Indels
                                                                                                         elongatus)
                                                               OrderedlocusNames=t1r1235;
Synechococcus elongatus (Thermosynechococcus elongatus
Bacteria; Cyanobacteria; Chrococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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25-OCT-2004 (TrEMBLrel. 28, Last seq
25-OCT-2004 (TrEMBLrel. 28, Last ann
4Mpothetical protein.
OrderedLocusNames=DP2570;
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Matches 6; Conservative
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                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                              NCBI_TaxID=32046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=84980;
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EMBL, ABAD3148; AAM25148.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.6%; Score 27; DB 2; Length 854; 29.2%; Pred. No. 5.8e+02; Live 0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.5%; Score 26; DB 2; Length 132; llarity 29.2%; Pred. No. 1.7e+02; Conservative 0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermoanaerobacter tengcongensis.
Bacteria, Firmicutes, Clostridia, Thermoanaerobacteriales,
                                                    InterPro; IPR003593, AAA ATBASE.
InterPro; IPR003593, AAA ATBASE.
InterPro; IPR003593, FAAA ATBASE.
InterPro; IPR003593, FAAA ATBASE.
InterPro; IPR0008984; SMAD FHA.
InterPro; IPR0005984; SMAD FHA.
InterPro; IPR0005984; FAAD FHA.
INTERPOSITE; PSCO005; FAAD FHA.
INTERPOSITE; PSCO006; FAAD FHA.
INTERPOSITE; PSCOO06; FAAD FHA.
INTERPOSITE FAAD FHA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8DJI8 PRELIMINARY; PRT; 246 AM. Q8DJI8; 01-MAR-2003 (TrEMBLrel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermoanaerobacteriaceae; Thermoanaerobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 AA
GO; GO:0000166; F:nucleotide binding; IEA.
GO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 NGTFVNGVRVDSAVLRDGDVVTIG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 NGTFVNGKRVKVARIKNGDIITLG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 NGTFXXXXXXXXXXXGDXXXXG 56
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InterPro; IPR00253; FHA.
InterPro; IPR008984; SMAD_FHA.
Ffam; PF00498; FHA; 1.
SMART; SM00240; FHA; 1.
PROSITE; PS50006; FHA_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FHA-domain-containing proteins. OrderedLocusNames=TTE1969;
                                      transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 29.2 nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Beet Local Similarity
7; Conserve
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                               GO:0006810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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STRAIN=CDC-1573;
PubMed=15039331; DOI=10.1128/IAI.72.4.2088-2100.2004;
Fletcher L.D., Bernfield L., Barniak V., Farley J.E., Howell A.,
Knauf M., Ooi P., Smith R.P., Weise P., Wetherell M., Xie X.,
Zagursky R., Zhang Y., Zlotnick G.W.;
"Vaccine potential of the Neisseria meningitidis 2086 lipoprotein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                          Thomson N. Charler K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
Rabbinowitesh B., Rajandream M.A., Rutherford K.M., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417.141-147(2002).
EMBL; AL939127; CAA20163.1; -.
PIR; T34986; T34986.
HSSP, Q50769; INYO.
                                                                                                                                                                                                                                                                       Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.5%; Score 25; DB 2; Length 22C 26.3%; Pred. No. 5.1e+02; ative 1; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 AA; 22362 MW; 78C08D7932B12C32 CRC64;
                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TIEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Lipoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 AA
                        95 NGTFNAKEVYITGTLGSGNAARTG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR0007082; BIGH3 FAS1.
PFan; PF02469; Fasciclin; T.
SMART; SMO0554; FASI; 1.
                                                                                                                                                                      Created)
                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 NGTFXXXXXXXXXXGD 51
                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-OCT-2003 (TrEMBLrel. 25, Putative secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50213; FAS1; 1.
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Best Local Similarity 26.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningītidis.
                                                                                                                                                                                                                                                      ORFNames=SC4A2.11c;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hopwood D.A.;
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                                                                                                                                                086667;
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                                                                                                                             086667
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                                                                                     RESULT 13
086667
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                                                                                                                                                                                                                                                                                                                                                                                           DECEMBER 210633 / Serotype 03:K6;

MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;

Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";

Lancet 1361:743-749(2003).

EMBL, AP005078; BAC59857.1; -.

Complete proteome; Hypothetical protein.

SEQUENCE 598 AA; 64664 MW; 3C41591D8AB218A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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BMBJ. AF288477; AAQ14336.1; -.
GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA
GO; GO:0009405; P:pathogenesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21981893; PubMed=11986271;
Feng S., Hodzic E., Kendall L.V., Smith A., Freet K., Barthold S.W.;
"Cloning and expression of a Helicobacter bilis immunoreactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Epsilonproteobactería; Campylobacterales;
Helicobacteraceae; Helicobacter.
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                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
VCBI_TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 26.5%; Score 26; DB 2; Length 598; Similarity 31.6%; Pred. No. 7.4e+02; 6; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1543 AA; 167034 MW; 6CADA242FFF4297E CRC64;
                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q71SNS;
C5-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                           598 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1543 AA
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InterPro; IPR004311; Put vacuo_cyttox.
Pfam; PF03797; Autotransporter; 1.
Pfam; PF03077; VacA2; 1.
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                                                                                                                                                                      Created)
                                                                                                                             PRT;
||||
187 NGTFVAGKKITFAELRSGD 205
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                                                                                                                                                           01-JUN-2003 (TYEMBLrel. 24, C
01-JUN-2003 (TYEMBLrel. 24, I
01-JUN-2003 (TYEMBLREL. 24, I
HYPOCHALICAL DICCEIN UP1594.
OrderedLocusNames-VP1594;
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Best Local Similarity 25.07
Best Local 6; Conservative
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                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                       Vibrio parahaemolyticus.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Q71SN5

RESULT 12

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Matches

SEQUENCE

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Gaps

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Length 220;

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Fraser C.M.;
                                         Awram
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOI=10.1128/JB.184.10.2709-2718.2002;
Umelo-Njaka E., Bingle W.H., Borchani F., Le K.D., Awram P., Blake T.,
Nomellini J.F., Smit J.;
                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 1-21; 646-660 AND 1021-1025. STARINS-ATCC 19089 / CB15; MEDLINE=93007489; Pubmed=1393820; Gilchrist A., Fisher J.A., Smit J.K.; Milcheride sequence analysis of the gene encoding the Caulobacter creecentus paracrystalline surface layer protein."; creecentus paracrystalline surface layer protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
NCBI_TaxID=155892;
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                                                                                                                                      25.5%; Score 25; DB 2; Length 260; 25.0%; Pred. No. 6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.5%; Score 25; DB 2; Length 359; 25.0%; Pred. No. 8.2e+02;
                                                                                                                                                                               18; Indels
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                                                                              <1 260 lipoprotein.
260 AA; 27563 MW; 8CC49D53851B635F CRC64;</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                               359 AA
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                                                                                                                                                                                                                                                          NGTLTLSAQGAEKTYGNGDSLNTG 71
                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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Infect. Immun. 72:2088-2100(2004)
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NCBI_TaxID=155892;
                  EMBL; AY330406; AAR84481.1; -
                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Truncated S-layer protein.
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                                                                                                                                                                               Conservative
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260
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                                                                                                                                                         Local Similarity
les 6; Conserv
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                                       Lipoprotein.
NON TER
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OPRIMI
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation — the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch)
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MEDLINE-98292737; PubMed-9620954;

MEDLINE-9829737; PubMed-
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STRAIN=ATCC 19089 / CB15;

STRAIN=ATCC 19089 / CB15;

MEDLINE=21170568; Dubmed=11259647; DOI=10.1073/pnas.061029298;

MEDLINE=211705698; Dubmed=11259647; DOI=10.1073/pnas.061029298;

Nicrman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Bisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

Podson R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Hadt D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,

Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,

Ermoleava M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Bingle W.H., Awram P.A., Nomellini J.F., Smit J.K.;
"The secretion signal of C. crescentus S-layer protein is located in the C-terminal 82 amino acids of the molecule.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
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STRAIN-ATCC 19089 / CB15;
MEDLINE=89008099; PubMed=3049545;
Figher J.A., Smit J.K., Agabian N.;
"Transcriptional analysis of the major surface array gene of
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1025 AA; 98001 MW; AD7A326E1363D8AC CRC64;
                                                                                                                                                                                   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
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Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
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Calcium-binding; Cell wall; Complete proteome;
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Interpro, IPR011049; Serralysn Tike C.
Pfam; PF00353; HemolysinCabind; 3.
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EMBL; AF193063; AAF19365.1; -.
EMBL; AE005779; AAK22991.1; ALT_INIT.
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INIT MET 0 0 SEQUENCE 1025 AA; 98001 MW; AD7,
[2]
REVISIONS TO 376; 636 AND 842-843.
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Conservative
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les 5; Conserv
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SEQUENCE FROM N.A.
                         STRAIN=ATCC 23344;
SEQUENCE FROM N.A
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01-OCT-2000
01-MAR-2003
PilV2.
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Q9KHW4;
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Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.

Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.

BREMEL, M622B911, CARS-2247.1;

CO; GO:0016021; Ciintegral to membrane; IEA.

GO; GO:0016021; F:ATP binding; IEA.

GO; GO:0016820; F:ATP binding; IEA.

GO; GO:0016820; F:Hydrolase activity, coupled to transmembrane m. .; IEA.

GO; GO:0016820; F:Hydrolase activity, acting on acid anhydrid. .; IEA.

GO; GO:0016820; F:Hydrolase activity, acting on acid anhydrid. .; IEA.

GO; GO:0006812; P:cation transport; IEA.

GO; GO:0008152; P:matabolism; IEA.

InterPro; IPR006089; Cation_ATPase.

InterPro; IPR006089; Cation_ATPase.

InterPro; IPR006089; Cation_ATPase N.

InterPro; IPR008091; EL-EZ ATPase N.

InterPro; IPR008091; EL-EZ ATPase N.

Pfam; PF00699; Cation_ATPase N.

Pfam; PF00612; EL-EZ ATPASE.

PRINTS; PR00112; NAMATTASE.

PRINTS; PR00112; NAMATTASE.

PRINTS; PR00112; NAMATTASE.
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Saccharomycetales; Saccharomycetaceae; Pichia.
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Burkholderia mallei ATCC 23344.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
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                  Query Match 25.5%; Score 25; DB 1; Length 1025; Best Local Similarity 25.0%; Pred. No. 2.2e+03; Matches 6; Conservative 0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00154; ATPASE E1 E2; UNKNOWN 1.
SEQUENCE 1105 AA; 122926 MW; 4878904DF7ECF50A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Thiamine biosynthesis protein This, putative.
                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                      PRT; 1105 AA
                                                                                                                                                       266 NDTFVAGEVAGAATLTVGDTLSGG 289
                                                                                                            33 NGTFXXXXXXXXXXXGDXXXXG 56
                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27,
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Pichia farinosa (Yeast).
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                                                                                                                                                                                                                                                                                                                                                                                  P-type ATPase.
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Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E., Feldblyum T., Ulrich R.L., Ronning C.M., Brinkec L.M., Daugherty S.C., Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M., Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N., Skructural flexibility in the Burkholderia mallei genome."; "Structural flexibility in the Burkholderia mallei genome."; EMBL, CP000010; Au148294.1; "BEL, CP000010; Au148294.1; "S64B131908DABFE CRC64;
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Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D.,
Peltuell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
Songsivials S., Stevens K., Tumapa S., Vesaratchaver M.,
Mhitchead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.,
"Genomic plasticity of the causative agent of melioidosis,
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Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
EMBL: BX571965; CAH37163.1; -
SEQUENCE 65 AA; 6572 MW; 5364B131908DA8FE CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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Name=this; ORFNames=BPSL3153;
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Reltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., M., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Mulie S., O'Gaora P., Parry C., M., Complete genome sequence of a multiple drug resistant Salmonella REMBL, ARC180691; A. R. InterPro, InterPro, Shifflon N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella enterica subsp. enterica serovar Paratyphi C.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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PubMed=14688076; DOI=10.1128/IAI.72.1.22-28.2004;
Tam C.K.P., Hackett J., Morris C.;
"Salmonella enterica serovar Paratyphi C carries an inactive
                                                                                                                                                                                                                                                                                                                                     24.5%; Score 24; DB 2; Length 435; 25.0%; Pred. No. 1.8e+03; ive 0; Mismatches 18; Indels
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25.0%; Pred. No. 1.9e+03;
ative 0; Mismatches 18; Indels
 MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
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EMBL; AY249242; AAP83041.1; -.
InterPro; IPR007001; Shufflon.N.
Pfam; PF04917; Shufflon.N; 123098601188B5F6 CRC64;
                                                                                                                                                                                                                                                                                                        435 AA; 46432 MW; C11F161143A93F79 CRC64;
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1-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Transferrin binding protein B subunit (Fragment).
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Complete proteome.
SEQUENCE 435 AA: 46412 MM
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STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; Pubdcd=12644504;
MEDLINE=22531367; Pubdcd=12347.2003;
DOI=10.1128/JB185.7.Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
                                                                                                                STRAIN=serovar Dublin;
MEDLINE=2934313; PubMed=14580391; DOI=10.1016/j.micpath.2003.08.001;
MEDLINE=29343013; PubMed=14580391; DOI=10.1016/j.micpath.2003.08.001;
MORTIS C., Tam C.K.P., Wallis T.S., Jones P.W., Hackett J.;
"Salmonella enterica serovar Dublin strains which are Vi antigen-positive use type 1VB pili for bacterial self-association and human intestinal cell entry.";
Microb. Pathog. 35:279-284(2003).
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MEDLINE=98087429; PubMed=9427557; DOI=10.1016/S0378-1119(97)00466-6;
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                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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"Molecular cloning, nucleotide sequence, and function of a site-
specific recombinase encoded in the major 'pathogenicity island'
Salmonella typhi.";
Gene 202:139-146(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 434;
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STRAIN=servovar Dublin;
Morris C.J., Hackett J.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF247502; AAF81218.1; -.
InterPro, IPR077001; Shufflon N.
Pfam; PF04917; Shufflon N: 11.—
SEQUENCE 434 AA; 46136 MW; 0273A4153BDD3518 CRC64;
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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25.0%; Pred. No. 1.8e+03;
live 0; Mismatches 18;
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NCBI_TaxID=601;
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               Salmonella dublin.
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                                                                                                                                                   MEDLINE=20105048; PubMed=10844690;
Linz B., Schenker M., Achtman M.;
"Frequent interspecific genetic exchange between commensal Neisseriae
and Neisseria meningitidis.";
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MEDIJUE=Z03048; PubMed=10844690;
Linz B., Schenker M., Achtman M.;
"Frequent interspecific genetic exchange between commensal Neisseriae
                                                                                                                                                                                                                                                                                                                                    MEDLINE-1221108; PubMed=11287631; DOI=10.1073/pnas.061386098;
Zhu P., van der Ende A., Falush D., Brieske N., Morelli G., Bodo L.,
Popovic T., Schuurman I.G.A., Adegbola R.A., Zurth K., Gagneux S.,
Platonov A.E., Riou J.Y., Caugant D.A., Nicolas P., Achtman M.;
Fit genotypes and escape variants of subgroup III Neisseria
meningitidis during three pandemics of epidemic meningitis.";
EMBL; AJ276928; CAC21592.1;
CG; GG:0016020; C:membrane; IEA.

GG; GG:0016020; C:membrane; IEA.

GG; GG:0004998; F:transferrin receptor activity; IEA.
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GO; GO:0016020; Camembrane; IEA.
GO; GO:0004998; F:transferrin receptor activity; IEA.
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Neisseriaceae, Neisseria.
                        Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.5%; Score 24; DB 2; Length 682; 25.0%; Pred. No. 2.7e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        682 AA; 73652 MW; D951B8868FCDD7D6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            574 NGTLTADNRQAATFTIVGDIEGNG 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 NGTFXXXXXXXXXXXGDXXXXG 56
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01-OCT-2000 (TrEMBLrel. 15, Last seq
                                                                                                                                                                                                                                                Mol. Microbiol. 36:1049-1058(2000).
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                                              Neisseriaceae; Neisseria.
NCBI_TaxID=487;
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nes 6; Conservative
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meningitidis.
                                                                                                          SEQUENCE FROM N.A.
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SEQUENCE
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MEDLINE=20305048; PubMed=10844690;
Linz B., Schenker M., Achtman M.;
"Frequent interspecific genetic exchange between commensal Neisseriae
                                                                                                           Gaps
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BMBL, AJZ76927, CAC215911.; -...
GO, GO:0016020; C:membrane; IEA.
GO, GO:0004998; F:transferrin receptor activity; IEA.
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MEDLINE=21221108; PubMed=11287631; DOI=10.1073/pnas.061386098;
MEDLINE=21221108; PubMed=11287631; DOI=10.1073/pnas.061386098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis.
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales;
Neisseriaceae, Neisseria.
NCBI_TaxID=487;
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25-OCT-2004 (Rel. 45, Last annotation update)
Transferrin-binding protein 2 precursor (TBP-2).
Name=tbpB; Synonyma=tbp2; OrderedLocusNames=NWA2025;
Neisseria meniagitidis (serogroup A).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                                                       Length 684;
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684 AA; 73610 MW; 13D6B69FBDC5A425 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Transferrin binding protein B subunit (Fragment).
                                                 24.5%; Score 24; DB 2; 1
25.0%; Pred. No. 2.7e+03;
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25.0%; Pred. No. 2.8e+03;
                                                                                                        0; Mismatches
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                                                                                                                                                               33 NGTFXXXXXXXXXXXXG 56
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01-MAR-2001 (TrEMBLrel. 16, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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Best Local Similarity 25.0°
Matches 6; Conservative
                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                       SEOUENCE FROM N.A.
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MEDITRE=22031233; PubMed=12033788; DOI=10.1006/viro.2002.1408; MEDITRE=22031233; PubMed=12033788; DOI=10.1006/viro.2002.1408; Chuchird N., Nishida K., Kawasaki T., Fujie M., Usami S., Yamada T.; A. variable region on the chlorovirus CVK2 genome contains five copies of the gene for Vp260, a viral-surface glycoprotein."; Virology 295:289-298(2002).

Which AB063108; BAB83469-1; -. Peam; PP06598; Chlorovi GP Frt; 14.

SEQUENCE 1464 AA; 149988 MW; ECCDA711437B6F5D CRC64;
                                                                                                                                                                                           Linz B., Schenker M., Achtman M.; "Frequent interspecified genetic exchange between commensal Neisseriae and Neisseria meningitidis." Mol. Microbiol. 36:1049-1058(2000).
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Zhu P., van der Ende A., Falush D., Brieske N., Morelli G., Bodo L.,
Popovic T., Schuurman I.G.A., Adegbola R.A., Zurth K., Gagneux S.,
Platonov A.E., Riou J.Y., Caugant D.A., Nicolas P., Achtman M.;
"Fit genotypes and escape variants of subgroup III Neisseria
meningitidis during three pandemics of epidemic meningitis.";
Proc. Natl. Acad. Sci. U.S.A. 98:5234-5239(2001).
EMBL, AJ776919; CAC21583.1;
GO; GO:0016020; C:membrane; IEA.
IIEA.
InterPro. IPR001677; Transferrin_bind.
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Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
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Similarity 25.0%; Pred. No. 2.88+03;
6; Conservative 0; Mismatches 18. ThAnh
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Last annotation update)
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Pred. No. 5.7e+03;
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                                                                                                                                                               MEDLINE=20305048; PubMed=10844690;
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   Neisseriaceae; Neisseria
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                                     NCBI_TaxID=487;
                                                                                                                                 STRAIN=25642;
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Q57226
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OC OX SERVICE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- FUNCTION: Acts as a transferrin receptor and is required for transferrin utilization (By similarity).
-1- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome; Lipoprotein; Outer membrane; Palmitate; Receptor;
                                                                                                                                                                                                                         "Human antibody responses to A and C capsular polysaccharides, IgAl protease and transferrin-binding protein complex stimulated by infection with Neisseria meningitidis of subgroup IV-1 or ET-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                PERAINS 22491 / Serogroup A / Serotype 4A;

MEDLINE=2022556; PubMed=10761919; DOI=10.1038/35006655;

MEDLINE=2022556; PubMed=10761919; DOI=10.1038/35006655;

METAILI J. Ackhran M., James K.D., Bentley S.D., Churcher C.M.,

Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd & Bajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

Whitehead S., Spratt B.G., Barrell B.G.,

"Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      By similarity.

Transferrin-binding protein 2.

N-palmitoyl cysteine (Probable).

S-diacylglycerol cysteine (Probable).

8-diacylglycerol cysteine (Probable).
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Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                                                  STRAIN=Z2491 / Serogroup A / Serotype 4A;
Brieske N., Quentin-Millet M.-J., Schenker M., Schnibbe T.,
Achtman M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 24; DB 1; Length 698; Pred. No. 2.8e+03;
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                                                                                                                                                                                                                                                                                                                                   complex.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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21 21 N-E
21 21 S-G
698 AA; 75176 MW; 6
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25.0%;
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           meningitidis Z2491.";
Nature 404:502-506(2000).
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Neisseriaceae; Neisseria
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Best Local Similarity
                                                                                               SEQUENCE FROM N.A.
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                              NCBI_TaxID=65699;
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SIGNAL
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Chlamydia trachomatis.
Bacteria, Chlamydiae; Chlamydiales, Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
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Bacteria; Chlamydiae; Chlamydiales; Chlamydia.
NCBI_TaxID=813;
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                                                  STRAIN=B2f;
Hsieh Y.-H., Bobo L.D.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AR070284; AR025254.1; -.
NON TER 1 1 2 2
NON TER 22 22
SEQÜENCE 22 AA; 2425 MW; B102482844167521 CRC64;
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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF070276; AAC25246.1; -.
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Haish: Y.-H., Bobo L.D.;
Submitted (1701-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AR070272; AAC25242.1; -
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
Major outer membrane protein (Fragment).
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Last annotation update)
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Pred. No. 1.8e+02;
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100.0%; Pred. No. ____
0; Mismatches
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
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Best Local Similarity 100.
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Best Local Similarity
Matches 4; Conserv
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SEQUENCE FROM N.A.
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Q9R8L6
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Minfect. Dis. 172:568-272(1995).
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"DNA sequence polymorphism of the Chlamydia trachomatis ompl gene.";
J. Infect. Dis. 168:1225-1230(1993).
EMBL; S66728; AB28611.1; -.
NON TER 22 22 22
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Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                                                     Chlamydia trachomatis.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
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Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.5%; Score 23; DB 2; Length 22; 100.0%; Pred. No. 1.8e+02; tive 0; Mismatches 0; Indels
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01-WAY-2000 (TrEWBLrel. 13, Created)
01-WAY-2000 (TrEWBLrel. 13, Last sequence update)
01-UJV-2001 (TrEMBLrel. 17, Last annotation update)
Major outer membrane protein (Fragment).
                                                01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1998 (TrEMBLrel. 08, Last annotation update) Major outer membrane protein (Fragment).
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MEDLINE=94044912; PubMed=7901288;
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Best Local Similarity 100.0.
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MEDLINE=21109142; PubMed=11162839; DOI=10.1006/viro.2000.0753; MEDLINE=21109942; PubMed=11162839; DOI=10.1006/viro.2000.0753; Ghezzi S., Menzo. S., Brambilla A., Panina Bordignon P., Lorini A.L., Clementi M., Poli G., Vicenzi E., Trinibition of R5X4 dualtropic HIV-1 primary isolates by single T. Chemokine co-receptor ligands."; Virology 280:553-261(2001).

R GO, GO:0016021; C:integral to membrane, IEA.
R GO, GO:0019031; C:integral to membrane, IEA.
R GO, GO:0019031; C:viral capsid; IEA.
R GO; GO:0005198; F:structural molecule activity; IEA.
R GO, GO:0005198; F:structural molecule activity; IEA.
R HOS GO:0005198; F:structural molecule activity; IEA.
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                                                                       Major outer membrane protein (Fragment).
Chlamydia trachomatis.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
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NON TER 31 31
SEQUENCE 31 AA; 3396 MW; 1FE12AAOF6C50B9A CRC64;
                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein V4 region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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Bacteria, Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
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Bacteria, Chlamydiae, Chlamydiales, Chlamydiaceae, Chlamydia.
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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF070248; AAC25218.1; -.
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Haieh Y.-H., Bobo L.D.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF070268; AAC25238.1; -
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SEQUENCE 22 AA; 2425 MW; B102482844167521 CRC64;
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22 AA; 2425 MW; B102482844167521 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence,
U-MAY-2000 (TrEMBLrel. 13, Last annotati
Major outer membrane protein (Fragment)
Name=omp-1;
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Search completed: February 24, 2005, 15:23:35 Job time : 113.715 secs
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35 NGTF 38
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A Ghezzi S., Menzo S., Brambilla A., Panina Bordignon P., Lorini A.L.,
Clementi M., Poli G., Vicenzi E.;
Tinhibition of RX4 dualtropic HIV-1 primary isolates by single
Tremokine co-receptor ligands.";
Virology 280:253-261(2001).
M. EMBL, AR33321; AAK21196.1;
M. GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; C:viral envelope; IEA.
GO; GO:0019028; P:structural molecule activity; IEA.
InterPro; IPR00515; GP120.
M. PADS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
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MEDIJIRE=21109142; PubMed=11162839; DOI=10.1006/viro.2000.0753;
MEDIJIRE=21109142; S., Brambilla A., Panina Bordignon P., Lorini A.L.,
Clementi M., Poli G., Vicenzi E.;
"Inhibition of RSX4 dualtropic HIV-1 primary isolates by single
chemokine co-receptor ligands.";
Virology 280:253-261(201)
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Pred. No. 2.6e+02;
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein V4 region (Fragment).
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein V4 region (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                             Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Gaps
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"Diversity of laccase genes from basidiomycetes in a forest soil.";
Soil Biol. Biochem. 36:1025-1036 (2004).
BISBL; AJ540279; CAD62542.1;
BISSP; Q97780; 1A65.
GO; GO:0008471; F:laccase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
Oxidoreductase.
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                                                                                                                                                uncultured basidiomycete.
Bukaryota; Fungi; Basidiomycota; environmental samples.
NCBI_TaxID=175244;
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               070U14;
070U14;
05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Laccase (EC 1.10.3.2) (Fragment).
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100.0%; Pred. No. 3.4e+02;
tive 0; Mismatches 0;
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February 24, 2005, 15:03:10; Search time 140.537 Seconds (without alignments) 184.386 Million cell updates/sec
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67 US-09-936-956-19 336 1 WIFGRNPACDYHLGNISRLS.....QKVEKNSNQLLSQGDEITVG 2105692 seqs, 386760381 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Scoring table: Sequence: Searched:

Total number of hits satisfying chosen parameters:

2105692

Post-processing: Minimum Match 0% Maximum Match 100% Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries

geneseqp1980s:*
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geneseqp2005s:* geneseqp2003as:*geneseqp2003bs:* A_Geneseq_16Dec04: geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Abp54942 Saccharom Abr53872 Protein 8 Abu61612 Yeast SPK Adk64880 Disease t Disease t Candida a Candida a Bacterial Bacterial Pseudomon pro aci Chf C glutami Mycobacte Mycobacte Human nov Human nov pro Aaw73894 Yeast MEC Aaw26664 Yeast che dia Human Novel Human Human Human Human Human Amino Human Description Abp73798 Ads44244 Adn19646 Abo68456 Aau15856 1 Abu54925 1 Abm83354 1 Abm83353 1 Abm83352 1 Aab93182 1 Abb97233 1 Aag89798 Aaw32352 Aaw32420 Aab03445 SUMMARIES ABP54942 ABR53872 ABU61612 ADK64880 ABM83353 ABM83352 AAB93182 AAG89798 AAW32352 AAW32420 AAB03445 ABP73798 ADS44244 ADN19646 AB068456 AAU15856 ABU54925 ABM83354 AAB83843 AAB20219 8 Length Query Score Result Š

Myc	Aav38957 M. tuberc		Aaw72886 Mycobacte	Aay21903 Amino aci	Aam50735 Mycobacte	Aam48994 Human Chk	Adl32563 Human Chk	Aag68375 Human Chk	Aay06204 Human che	Novel	Human	Aam48995 Human Chk	Abg30701 Human che	Adl32561 Human Chk	Adm72213 Human TAS	Ado44010 Amino aci	Adq09232 Human CHE	Adn61455 Human KPP
AAW64292	AAY38957	AAY39094	AAW72886	AAY21903	AAM50735	AAM48994	ADL32563	AAG68375	AAY06204	AAY05765	AAM48996	AAM48995	ABG30701	ADL32561	ADM72213	ADO44010	ADQ09232	ADN61455
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148	148	148	161	162	162	514	514	542	543	543	543	543	543	543	543	543	543	286
23.7	23.7	23.7	23.7	23.7	23.7	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.9	22.9
79.5	79.5	79.5	79.5	79.5	79.5	77	77	77	77	77	77	77	77	77	77	77	77	7.7
26	7 8	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

cycle checkpoint gene; yeast; radiation resistance; detection; Weinert TA; (UNIW) UNIV WASHINGTON. (UYAR-) UNIV ARIZONA. (HUTC-) HUTCHINSON CANCER RES CENT FRED Plon SE, Groudine MT, Hartwell LH, AAW73894 standard; protein; 776 AA 92US-00882051. 92US-00884426. 93WO-US004458. 94US-00198446. 97US-00870693. Yeast MEC2 protein sequence (first entry) Saccharomyces cerevisiae Cell cycle check G2/M checkpoint 14-MAY-1992; 12-MAY-1993; 18-FEB-1994; 06-JUN-1997; 12-MAY-1992; 08-APR-1999 US5866338-A. 02-FEB-1999 AAW73894; AAW73894 CCCCCCXXXX11XXBXX1XXBXXBXBXX6XDXXXXXXXXXXCCCCCCCXXXXX1XXBXXAXX

WPI; 1999-141919/12.

N-PSDB; AAX01275

Nucleotide sequences that hybridise to huRAD cDNA - method for isolating human checkpoint cDNA, and antibody to CDC34.

Example 4; Col 89-96; 73pp; English.

This sequence is the yeast MEC2 protein. The DNA encoding this sequence is necessary for \$2/M cell cycle checkpoint control. This sequence was identified using the method of the invention for isolating a human checkpoint cDNA that is capable of restoring growth at a restrictive temperature in a yeast test cell, where the yeast test cell comprises a genome having a first gene that forms a DNA strand break at a restrictive temperature and a second gene that fails to induce a cell cycle arrest in response to the DNA strand break, whereby the growth of the yeast test

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cell is inhibited at the restrictive temperature, comprising: (a) obtaining a human cDNA library comprising several human cDNA clones individually into plasmid vectors containing a selectable marker gene; (c) transforming a culture of the yeast test cells with the plasmid vectors from the preceding step; (d) selecting for yeast test cells transformed with the selectable marker gene; (e) growing the selected transformants at the restrictive temperature and isolating a candidate transformant capable of growing at the restrictive temperature; and (f) identifying the human cDNA carried by the candidate transformant and determining that the human cDNA carried by the candidate transformant and determining that the human cDNA carried by the candidate transformant and determining that the second gene. The nucleotide sequence of huRADcompB can be used to
                                                                                                                                                                                                                                         WTFGRNPACDYHLGNISRLSNKHPQILLGEDGNLLLNDISTNGTWLNGGKVEKNSNQLLS 125
                                                                                                                                                                                                                             59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide sequence capable of hybridiaing with huCDC34 - which is human checkpoint gene, useful to increase sensitivity of tumour cells to chemotherapeutic drugs or radiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEC2; cell cycle; checkpoint gene; yeast; DNA damage; cancer; therapy.
                                                                                                                                                                                                                            1 WTFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLS
                                                                                                                                                                                                          Gaps

    .776
/note= "in the Sequence Listing MEC2 terminates at

                                                                                                                                                                                                        1;
                                                                                                                                                                               Score 313.5; DB 2; Length 776;
Pred. No. 2.4e-33;
0; Mismatches 6; Indels 1:0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plon SE, Hartwell LH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUTCHINSON CANCER RES CENT FRED.
                                                                                                                                                                                                                                                                                                                                                                                                                     Yeast checkpoint control protein MEC2.
                                                                                                                                         confer radiation resistance on a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                             AAW26664 standard; protein; 821 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-00198446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92US-00882051.
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93WO-US004458.
                                                                                                                                                                                   93.3%;
89.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   residue 775"
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Groudine MT, Weinert TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae.
                                                                                                                                                                                                       61; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        (revised)
                                                                                                                                                                                                                                                                                     QGDEITVG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNIV ARIZONA
                                                                                                                                                                                                                                                                      60 QGDEITVG 67
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                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT91040.
                                                                                                                                                              Sequence 776 AA;
                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
25-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEB-1994;
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12-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5674996-A.
                                                                                                                                                                                                                                                                                                                                                                   AAW26664;
                                                                                                                                                                                                                                                 99
                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYAR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reducing growth of cancer cells comprises reducing Tyrosine Threonine Kinase (TTK) activity, useful in diagnosing and treating disorders with abnormal expression levels and activity of TTK, such as lung, colon,
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPK1; tyrosine threonine kinase; TTK; protein kinase; enzyme; mitotic checkpoint; colon cancer; breast cancer; tumour; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                 Length 821;
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                               . 9
                                                                                                                                                                                                                                                                                                                                                                              93.3%; Score 313.5; DB 2, 89.7%; Pred. No. 2.6e-33; ive 0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 77-78; 113pp; English
Example 4; Col 85-90; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chan VW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP54942 standard; peptide; 821 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae SPK1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-2001; 2001US-0271254P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prostate and ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jefferson AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 89.7 tes 61, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae
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|26 QGDEITVG 133
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N-PSDB; ABV73988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 QGDEITVG
                                                                                                                                                                                                                                                                                                                                               Sequence 821 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200268444-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP54942;
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to multiprotein complexes from eukaryotes. Proteins of the invention and DNA sequences encoding them are given in records ABR52588-ABR53903 and ACC60610-ACC61944 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins which is attached thereto from cells. Such protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful
The present sequence is the protein sequence of Saccharomyces cerevisiae PSFX1, a protein related to human tyrosine throomine kinase (TTK, see ABP54938). TTK polymucleotides and polypeptides of the invention encompass polymucleotides and polypeptides having sequence similarity or encompass polymucleotides and polypeptides having sequence similarity or the invention is based on the finding that TTK is differentially expressed in various forms of cancer. It provides methods for the identification of cancerous sells, especially heast cancer and colon cancer cells, by detection of expression levels of TTK, se well as diagnostic, prognostic and therapeutic methods. These methods can be used as the basis of tational tharapy. Assays for identifying molecules that modulate the activity of these genes in cancers, as well as methods of inhibiting tumour growth by inhibiting the activity of TTK are also
                                                                                                                                                                                                                                                                              66 WIFGRNPACDYHLGNISRLSNKHFQILLGEDGNLLLNDISTWGTWLNGQKVEKNSNQLLS 125
                                                                                                                                                                                                                                                              1 WIFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated protein complexes useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kuester BD;
                                                                                                                                                                                                               Score 313.5; DB 5; Length 821;
Pred. No. 2.6e-33;
0; Mismatches 6; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 2609; 17pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Multiprotein complex; eukaryote; drug target; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kruse UD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      i P, Krause R, K
Superti-Furga GD;
                                                                                                                                                                                                                                                                                                                                                                                                        ABR53872 standard; protein; 821 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein sequence #SEQ ID 2609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gavin A, Grandi P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-DEC-2001; 2001EP-00130253
                                                                                                                                                                                                                 93.3%;
89.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marzioch M, Schultz JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae.
                                                                                                                                                                                                                                        61; Conservative
                                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CELL-) CELLZOME AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2003-250078/25.
                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                   QGDEITVG
                                                                                                                                                                                        Sequence 821 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ACC61914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                ABR53872;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorder
                                                                                                                                                                provided
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                                                                                                                                                                                                                                         Matches
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The invention relates to detecting cancer (other than ovarian cancer) in a subject, comprising comparing the expression levels of tyrosine threonine kinase (TTK, a mitotic checkpoint game) polypeptide or polynucleotide in a test cell obtained from the subject and in a normal non-cancer cell, where an increase in the expression level of TTK protein or nucleic acid in the test cell compared to that in the normal cell, indicates the presence of cancer other than ovarian cancer. Also included are reducing growth of a cancerous cell (by contacting a cancerous cell with an amount of an agent effective to reduce TTK polypeptide activity in the cell), an assay for identifying a candidate agent that reduces growth of a cancerous cell (comprising: (i) detecting the activity of a TTK polypeptide in the presence of a candidate agent; and (ii) comparing
for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office. The complete document is available on CD-ROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                66 WIFGRNPACDYHLGNISRLSNKHFQILLGEDGNLLLNDISTNGTWLNGQKVEKNSNQLLS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comparing expression levels of tyrosine ynucleotide in a subject cell and a
                                                                                                                                                                                                                                                                                                                                                                                                          59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kinase polypeptide or polynucleotide in a subject cell and a
11, where an increase in the expression level in the test cell
                                                                                                                                                                                                                                                                                                                                                                                                          1 WTFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLS
                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                Length 821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yeast, tyrosine threonine kinase, TTK; cancer, cytostatic, mitotic checkpoint gene; SPK1.
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                             Score 313.5; DB 6;
Pred. No. 2.6e-33;
0; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chan VW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU61612 standard; protein; 821
                                                                                                                                                                                                                                                                                   93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-2002; 2002US-00081119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-FEB-2001; 2001US-0289813P.
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 8>....
Thes 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jefferson AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           normal cell, where an in
is indicative of cancer.
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QGDEITVG 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-456566/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yeast SPK1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ACA62264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REIN/) REINHARD
                                                                                                                                                                                                                         Sequence 821 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS2003045491-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reinhard C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU61612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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the activity of TTK polypeptide in the presence of a candidate agent relative to TTK polypeptide activity in the absence of the candidate agent, identifying an agent that reduces TTK activity (comprising: (i) contacting a cancerous cell displaying elevated expression of a TTK-encoding polynucleotide with a candidate agent; and (ii) determining the effect of the candidate agent on TTK polypeptide activity) and assessing the prognosis of a cancerous disease other than owarian cancer in a subject (comprising: (i) detecting expression of TTK-encoding polynucleotide in the test cancer cell of expression of TTK-encoding polynucleotide in the test cancer cell with a level of expression of the polynucleotide in the test cancer cell with a level of expression of TTK in the test cancer cell where the level of expression of TTK in the test cancer cell is indicative to the prognosis of the cancerous disease). The methods are useful for detecting cancer (other than ovarian cancer) in a subject, cancing growth of cancerous cells, identifying a candidate agent that reduces TTK activity and assessing the prognosis of a cancerous disease other than covarian cancer. The methods are also useful for determining the ability of a subject to respond to a particular therapy e.g. as a basis of rational therapy. The present sequence represents a closely related to protein to human TTK, in this case yeast SPKI (not defined)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 WTFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New proteins and protein complexes from eukaryotes, useful as targets in diagnosing or screening, or in diagnosing or screening for the presence of a disease or disorder, or a predisposition for developing a disease or disorder in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superti-Furga G, Kuester B, Schultz J;
P, Krause R, Kruse U, Merino A, Bauch A;
C, Rick J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 7; Length 821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disease treating protein complex-derived protein #1576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 2.6e-33;
0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.3%; Score 313.5;
89.7%; Pred. No. 2.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein complex; drug target; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADK64880 standard; protein; 821 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-DEC-2001; 2001EP-00130253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 89.7
Matches 61; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QGDEITVG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGDEITVG 67
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1, Grandi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-638460/61.
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 821 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADK64881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bauer A,
Marzioch
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The invention relates to novel protein complexes comprising a first and a second protein, or its derivative, fragment, homologue or variant. The proteins are selected from given protein complexes, which are not defined in the specification. The variants are encoded by nucleic acids that hybridize to the nucleic acids encoding the proteins under low stringency conditions. The protein complexes are useful as targets for an active agent of a pharmaceutical. These protein complexes are particularly useful as drugs targets for the treatment or preventing of a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject. These are also useful in screening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein components of the complex is useful for the manufacture of a medicament or prevention of a disease or disorder. This sequence corresponds to a protein of the invention. (Note: the sequence data for this patent did not form part of the printed specification but was obtained from the EPO in electronic format).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 WTFGRNPACDYHLGNISRLSNKHFQILLGEDGNLLLNDISTNGTWLNGQKVEKNSNQLLS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Growth inhibition; survival; pathogen; fungal infection; vulvovaginitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acid molecule and polypeptides essential for survival and growth of yeast candida albicans useful for treating candida albicans associated diseases and for identifying antifungal compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 WIFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 313.5; DB 7;
Pred. No. 2.6e-33;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Candida albicans essential growth protein #3.
                Disclosure, SEQ ID NO 3151, 13pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB03445 standard; protein; 699 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 93.3%;
Best Local Similarity 89.7%;
Matches 61; Conservative
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Logghe MG, Vialard JE;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 821 AA;
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The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by recombination, of a promoter replacement fragment with a heterologous promoter, so that expression of the second allele is regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells having both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene
The present sequence is a protein which is essential for the survival and growth of Candida albicans. This fungus causes infection, such as vulvovaginitis, in humans, particularly in those who are immunocompromised. The protein and its gene can be used to diagnose infection, and they can be used as targets for inhibiting the proliferation of the fungus. This protein and gene are particularly useful as they are thought to be species-specific
                                                                                                                                                                                                                                                                                           Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression
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                                                                                                                                                                                                                                 Gaps
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signal transduction, DNA replication; cell division, growth,
proliferation, Candida albicans, fungicide, antifungal.
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                                                                                                                                                                                        50.0%; Score 168; DB 3; Length 699; 53.6%; Pred. No. 1.4e-13; ive 8; Mismatches 22; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP73798 standard; protein; 699 AA
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20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
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NQGDEIAVG 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-566694/60.
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agent, an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian disease. (M1) is useful for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon compound catabolism, blosynthetic, transporter, transcriptional, translational, signal transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and for treating infection by C. albicans. The present sequence is that of an essential candida albicans protein used in the method of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                             28
to the resistance of a diploid fungus to an antifungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cold tolerance, heat tolerance; drought tolerance; herbicide, osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant DNA construct; transformed plant; improved plant property;
                                                                                                                                                                                                                                                                                                                                                          1 WIFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXL-LNDISTNGTWLNGOKVEKNSNQLL
                                                                                                                                                                                                                                                                                                                        5.
                                                                                                                                                                                                                                                                                       50.0%; Score 168; DB 5; Length 699; 53.6%; Pred. No. 1.4e-13;
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                                                                                                                                                                                                                                                                                                                        8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADS44244 standard; protein; 609 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-FEB-2002; 2002US-0360039P.
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                                                                                                                                                                                                                                                                                                       Local Similarity 53.6
nes 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 NOGDETAVG 130
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SLATER S C.
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                                                                                                                                                                                                                                                       Sequence 699 AA;
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(SLAT/)
(CHEN/)
(GOLD/)
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                                                                                                                                                                                                                                                                                                                        Matches
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant as a crop plant such as maize or soybean. The method of producing a transformed plant the such as maize or soybean. The method of producing a plant is a crop plant such as maize or soybean. The method of producing a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties. The recombinant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of combodydrate, nitrogen or phosphorus use and/or property modification of carbohydrate, nitrogen or property plant property and plant growth regulators, increased rate of content, improved ylath by modification of carbohydrate, nitrogen or property property and plant property plant growth regulators, increased rate of content, improved ylath by modification of carbohydrate, nitrogen or property property and plant property plant plant property plant property plant plant property plant property plant p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             providing improved plant growth and development under at least one giress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic
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119 RNDSDESENVVFLHGKSKGLKNLLKSSASSTFSNNFRHSSNGTFLNFVSESLIRLQFTDV 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 WIFGRNPACDYHLGNISRLSNKHFQI------LXXXXXXLLNDI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            format from USPTO at segdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::: ||| :|| || :|
179 IXERLAKNSRTILSNGDEIRIG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 -GOKVEKNSNOLLSOGDEITVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADN19646 standard; protein; 474 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-2003; 2003US-00369493.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 609 AA;
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ADN19646
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promoter functional in a plant cell, where the promoter comprising a microbial source. The invention also relates to a transformed plant comprising the recombinant bNA construct and a method of producing a comprising the recombinant bNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant source or soybean. The method of producing a transformed plant having an improved property comprises transformed plant, where the having an improved property comprises transformed plant, where the recombinant bNA construct and growing the transformed plant properties. The recombinant bNA construct is useful for improving plants with the polynucleotide or polypeptide is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, colerance to herbicides, extreme semble conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved plant growth and development under at least one stress condition, improved light production or improved galactomannan production or improved algain production or improved galactomannan production or improved the represents a bacterial polypeptide used in the production. This sequence represents a bacterial polypeptide used in the
                                                                                                                                                                                                                New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 GRSNTCNYQLLQFT-ASYKHFRVYSVLIDDDMDPLVYCEDQSSNGTFLNHRLIGKGNSVL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 GRNPACDYHLGNISRLSNKHFQILXXXXXXLLN-----DISTNGTWLNGQKVEKNSNQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                           The invention relates to a recombinant DNA construct comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.7%; Score 86.5; DB 8; Length 474; 33.3%; Pred. No. 0.01; ive 14; Mismatches 25; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     at segdata.uspto.gov/sequence.html
                                                                                                                                 Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa polypeptide #631.
                                                                                                                               Chen X,
                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 2299; 122pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABO68456 standard; protein; 558 AA.
                                                                                                                               Slater SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 LSQGDEITV 66
CAO Y.
HINKLE G J.
SLATER S C.
                                                                                     GOLDMAN B S
                                                                                                                                                                      WPI; 2004-061375/06
                                                                                                                               Hinkle GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 23; Conserv
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                                                                 CHEN X
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  CAOY/)
                                                                                   (GOLD/)
                                                               (CHEN/)
                        HINK/)
                                           SLAT/)
                                                                                                                               Cao Y,
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WO200155322-A2
                         02-AUG-2001
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                                                                                                                                                                                                                                          The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and theraphological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a companylaxis and treatment of pathological conditions resulting from a companylaxis and treatment of pathological conditions resulting from a companylaxis and treatment of pathological conditions as components of correction infection, for evaluating a compound, such as a polypeptide, confection of P. aeruginosa nucleic acid, as components of production of P. aeruginosa sequences or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa sequences or other sequences infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences or other sequences of Pseudomonas species using biochip technology. Sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed specification but, was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 TIGRGPDNDWVLPDPERLVSSRHCTILNRDGVYYLTDTSTNGVLVNAGHRLRRGNSEPL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; Alzheimer's disease; infection; ocular disorder; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TFGRNPACDYHLGNISRL-SNKHFQILXXXXXXLLNDISTNGTWL--NGOKVEKNSNQLL 58
                                                                                                                                                                Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment opathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.4%; Score 85.5; DB 7; Length 558;
33.3%; Pred. No. 0.017;
tive 13; Mismatches 30; Indel8 3; Gaps
                                                                                                    Bush D;
                                                                                                                                                                                                                    Disclosure; SEQ ID NO 17202; 455pp; English.
                                                                                                  Rubenfield MJ, Nolling J, Deloughery C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human novel secreted protein, Seg ID 809.
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                                                                          THERAPEUTICS CORP.
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          99US-00252991
                                   98US-0074788P.
98US-0094190P.
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Best Local Similarity 33.3%;
Thes 23; Conservative
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152 QDGETVRLG 160
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                                                                                                                           WPI; 2003-615309/58.
N-PSDB; ABD02027.
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                                                                         (GENO-) GENOME
          18-FEB-1999;
                                    18-FEB-1998;
27-JUL-1998;
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17-JAN-2001; 2001WO-US001341
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29-SEP-2000; 2000US-0236327P.
29-SEP-2000; 2000US-0236367P.
29-SEP-2000; 2000US-0236369P.
29-SEP-2000; 2000US-0236369P.
29-SEP-2000; 2000US-0236309P.
02-OCT-2000; 2000US-0237039P.
02-OCT-2000; 2000US-0237039P.
02-OCT-2000; 2000US-0237039P.
02-OCT-2000; 2000US-023703P.
03-OCT-2000; 2000US-023703P.
03-OCT-2000; 2000US-023703P.
03-OCT-2000; 2000US-023937P.
03-OCT-2000; 2000US-0241787P.
03-OCT-2000; 2000US-0241787P.
03-OCT-2000; 2000US-0241809P.
03-OCT-2000; 2000US-0241809P.
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03-OCT-2000; 2000US-0241809P.
03-NOV-2000; 2000US-024647P.
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2000US-0249210P.
2000US-0249211P.
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2000US-0249264P.
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01-DEC-2000; 2
05-DEC-2000; 2
05-DEC-2000; 2
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08-NOV-2000;
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Ruben SM;

Barash SC,

Rosen CA,

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The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to encoded secreted proteins. The nucleic acids and proteins are used to revenit treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a also used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (EILSA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hypotroliferative disorders e.g. cardiac carest, cerebrovascular disorders e.g. cherebral ischaemia, analyceneeis, nervous system disorders e.g. Alzheimer's disorders e.g. corneal infection, bacteria, viruses and fungi and ocular disorders e.g. corneal infection, con many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before capabilities, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, coffactors and other nutritional components. The present sequence represente a novel secreted protein of the invention. Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 WTFGRNPACDYHLGNISRLSNKHFQIL--XXXXXXLLNDISTNGTWLNGQKVEKNSNQLL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 WIIGRRRGCDLSFPSNKLVSGDHCRIVVDEKSGQVTLEDTSTSGTVINKLKVVKKQTCPL 99
                                                                                              New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; neural disorder; immune system disorder; renal disorder; muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; phyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antiinflammatory; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; haemostatic; antiarteriosclerotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Gaps
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                                                                                                                                                                                                     Claim 11; SEQ ID NO 809; 980pp; English
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                       2001-488783/53.
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                                                  N-PSDB; AAS25843
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2000US-0229287P.
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2000US-0229513P.
2000US-0231413P.
2000US-0234223P.
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2000US -0234997P
2000US -0235834P
2000US -0235327P
2000US -0235368P
2000US -0235368P
       2000US-0179065P.
2000US-0180628P.
2000US-0214886P.
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2000US-0218290P.
2000US-0220963P.
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2000US-0239935P.
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2000US-0225267P.
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02-OCT-2000; 2
02-OCT-2000; 2
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13-OCT-2000; 2
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20-OCT-2000; 2
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01-NOV-2000; 2
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05-SEP-2000; 2
08-SEP-2000; 2
1-SEP-2000; 2
21-SEP-2000; 2
25-SEP-2000; 2
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14-AUG-2000; 2
14-AUG-2000; 2
22-AUG-2000; 2
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08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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01-SEP-2000;
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14-AUG-2000;
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ROSEN C A. RUBEN S M. BARASH S C. (ROSE/) R (RUBE/) R (BARA/) E Barash SC; Rosen CA, Ruben SM,

WPI; 2003-147444/14 N-PSDB; ABX73184. New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or renal disorders.

Claim 11; SEQ ID NO 809; 402pp; English.

The invention relates to human novel polypeptides and their associated polynuclectides. The polypeptides and polynuclectides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g.

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nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders, quastrointestinal disorders, pulmonary disorders, cardiovascular disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial infarction) and cancerous diseases. Sequences ABUS4914-ABUS5699 and ABUS5748 represent human novel polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     scnmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL,
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
Patury S, Shi X, Suarez CJ;
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                                                                                                                                                                                                                                                                                                                                                   40 WIJGRRRGCDLSFPSNKLVSGDHCRIVVDEKSGQVTLEDISISGTVINKLKVVKKQTCPL
                                                                                                                                                                                                                                                                                                                             1 WIFGRNPACDYHLGNISRLSNKHFQIL -- XXXXXXLLNDISTNGTWLNGQKVEKNSNQLL
                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 0.014;
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12-SEP-2002; 2002US-0410260P.
                                                                                                                                                                                                                                                   Query Match 25.3%;
Best Local Similarity 34.8%;
Matches 23; Conservative
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N-PSDB; ACN42006.
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                                                                                                                                                                                                                 Sequence 426 AA
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used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, and autoimmune/inflammatory disorder, developmental disorders, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from NIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Money EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
  diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
                                                                                                                                                                                                                                                                                                                                                                                                                     38 WIIGRRAGCDLSFPSNKLVSGDHCRIVVDEKSGQVTLEDTSTSGTVINKLKVVKKQTCPL 97
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                                                                                                                                                                                                                                                                                                                                                                                              1 WIFGRNPACDYHLGNISRLSNKHFQIL--XXXXXXLLNDISINGTWLNGOKVEKNSNQLL
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                                                                                                                                                                                                                                                                                                                 25.3%; Score 85; DB 8; Length 572; 34.8%; Pred. No. 0.021; ive 6; Mismatches 35; Indels
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12-SEP-2002; 2002US-0410260P.
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Best Local Similarity 34.87
....nes 23; Conservative
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S. Shi X,
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                                                                                                                                                                                                                                                                            Sequence 572 AA;
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Claim 27; Page; 190pp; English.

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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp conclusive may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, and for somatic or germline invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from MIPO at www.wipo.int/pct/en/sequences/listing.htm
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Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Bider LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen BJ, Wu MC, Stuve LL;
Liagace RB, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
Patury S, Shi X, Suarez CJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Gaps
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12-SEP-2002; 2002US-0410260P.
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RESULT 18
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                             The invention relates to novel diagnostic and therapeutic polymucleotides selected from one of the 2722 sequences defined in the specification. A purintelectide of the invention may have a use in gene therappy. The human diagnostic and therapeutic polymucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine utoimmune/inflammatory disorder, developmental disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp confections caused by virus, bacteria, fungi or parasite. The dithp confections and also be used in genetic mapping, in identifying individuals committe biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from NIPO at www.wipo.int/pct/en/sequences/listing.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                       1 WIFGRNPACDYHLGNISRLSNKHFQIL - - XXXXXXLLNDISTNGTWLNGQKVEKNSNQLL 58
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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                                                                                                                                                                                                                                                         25.3%; Score 85; DB 8; Length 612; 34.8%; Pred. No. 0.023; ive 6; Mismatches 35; Indels
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, Otsuki
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A, Nagai K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB93182 standard; protein; 623 AA.
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Sugiyama T, Wakamatsu
            Claim 27; Page; 190pp; English
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11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
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hes 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                         QTGDVI 103
                                                                                                                                                                                                                                                                                                                                                   SQGDEI 64
                                                                                                                                                                                                                                  Sequence 612 AA;
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Ishii S,
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                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 17
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The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:

[a] an oligo-dr primer and an oligonucleotide comprises one of the 5602
complementary strand of a polymucleotide which comprises one of the 5602
nucleotide sequences defined in the specification, where the
coligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprises a sequence complementary to the
complementary strand of a polymucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polymucleotide comprises at least 15 nucleotides and the combination of
complementary strand of a polymucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence, where the
coligonucleotide comprises at least 15 nucleotides and the combination of
coligonucleotide which comprises a 15 nucleotides and the combination of
coligonucleotide whill-length cDNAs. The primers are also useful for the
capacitication and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers allow obtaining of the full-length
colligonucleotides, and sequences; AAB13628 and
AAH13633 to AAH13633 to AAH13632 represent human anino acid sequences; and AAH13632 represent
coligonucleotides.

Colig
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antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
neuroprotective; antiparkinsonian; protein therapy; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 WIIGRRRGCDLSFPSNKLVSGDHCRIVVDEKSGQVTLEDISTSGTVINKLKVVKKQTCPL
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Claim 8; SEQ ID NO 12128; 2537pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 623;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Asundi V, Zhang J,
I, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 85; DB 4;
Pred. No. 0.023;
6; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human protein SEQ ID NO: 501.
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Yang Y, Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-SEP-2001; 2001WO-US026015.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expressed sequence tag.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTGDVI 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention
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Local Si.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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complementary strand of a polymucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the nucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the comprises an oligonucleotide comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polymucleotide comprises a 1'-end sequence complementary to a polymucleotide comprises at 1'-end sequence, where the comprises at least 15 nucleotides and the combination of the 5'-end sequence 3'-end sequence; where the comprises at least 15 nucleotides and the combination of specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polymucleotides, particularly full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13631 to AAH13632 represent human anino acid sequences; and AAH13629 to AAH13632 represent complementation of the com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a FHAR1 polypeptide, which is a member of the RING finger protein family. FHAR1 is useful in the treatment of cancer, and as a vaccine for inducing an immunological response in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 WIFGRNPACDYHLGNISRLSNKHFQIL--XXXXXXLLNDISINGTWLNGQKVEKNSNQLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of a human ring finger protein designated FHAR1.
     oligo-dT primer and an oligonucleotide complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 85; DB 4; Length 652; Pred. No. 0.025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hurle MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB83843 standard; protein; 664 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 19; 28pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-DEC-2000; 2000WO-US033094.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.3%;
34.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 QTGDVI 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 652 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 SQGDEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                   The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTS). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. parkinson's disease. The present sequence is a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WIIGRREGODLSFPSNKLVSGDHCRIVVDEKSGQVTLEDTSTSGTVINKLKVVKKOTCPL 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WIFGRNPACDYHLGNISRLSNKHFQIL--XXXXXXLLNDISTNGTWLNGQKVEKNSNQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; primer; detection; diagnosis; antisense therapy; gene therapy.
An isolated polynucleotide for treating diseases associated with its encoded polypeptide such as cancer and multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto J;
T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5; Length 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.3%; Score 85; DB 5; Length 623
34.8%; Pred. No. 0.023;
ive 6; Mismatches 35; Indels
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Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayashi K, S
A, Nagai K,
                                                                                   Example 2; SEQ ID NO 501; 509pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human protein sequence SEQ ID NO:12100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB93168 standard; protein; 652 AA.
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T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAX-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
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les 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 623 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQGDEI
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mammal. FHAR1 polynucleotides may also be used as a diagnostic reagent through detection of mutations in the associated gene, and for chromosome localization studies, and tissue expression studies. FHAR1 antibodies are useful to isolate and to identify clones expressing the polypeptides, or to purify the polypeptides by affinity chromatography and to treat cancer
                                                                                                                                                 28
                                                                                                                                                             Checkpoint with forkhead associated domain and ring finger; Chfr; human; mitosis; cell cycle; tumour; diagnosis; antitumour; drug screening; ubiquitin-protein ligase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acid sequence of mitotic checkpoint gene encoding a checkpoint with forkhead-associated domain and ring finger protein, for diagnosing tumorigenic cells and in screening for anticancer drugs.
                                                                                                                                               1 WTFGRNPACDYHLGNISRLSNKHFQIL--XXXXXXLLNDISTNGTWLNGQKVEKNSNQLL
                                                                                                                        Gaps
                                                                                                                         2;
                                                                                               Score 85; DB 4; Length 664;
Pred. No. 0.025;
6; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                               Human Chfr (checkpoint with FHA and ring finger) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31. .103
/label= Forkhead-associated_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Ring_finger-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Met in U2OS cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            476. .641
/note= "cysteine-rich
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                                                                                                                                                                                                                                                                                     AAB20219 standard; protein; 664 AA.
                                                                                               ch 25.3%;
1 Similarity 34.8%;
23; Conservative 6
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N-PSDB; AAF30352.
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                                                                         Sequence 664
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                   mitosis;
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Matches
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c inactivated in 4 of 8 human cancer cell lines. In UZOS cells, a mutation was identified that caused a Val to Met amino acid substitution in the highly conserved C-terminal Cys-rich region of the Chfr protein. In the absence of the Chfr checkpoint, cells subjected to mitotic stress condensed their chromosomes despite failing to separate their chromosomes. Chfr may monitor centrosome separation. Inactivation of the chromosomes. Chfr may monitor centrosome separation. Inactivation of the chromosomes. Chfr may monitor centrosome separation. Inactivation of the chromosomes. Chfr may monitor centrosome separation. Inactivation of the increased sensitivity of cancer cells to antimitotic drugs. Polypeptides increased sensitivity of cancer cells to antimitotic drugs. Polypeptides comprising the present sequence, or sequences comprising at least amino acids 31-103, 303-346 and/or 476-641 of this sequence, are claimed. Claimed methods of determining the tumourigenic potential of a cell comprise examining the cell for the presence of Chfr expression or for the presence of Chfr expression indicating prediaposition to tumourigenesis upon exposure to mitotic stress). A diagnostic kit for detecting the cumourigenic potential of cell cells comprises may comprise a ligand that binds to Chfr, such as an antibody or its fragment. Inhibitors of Chfr are identified by monitoring their effect on Chfr expression, and are used to retard the growth of cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H1;
therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell cycle regulatory factor-encoding gene for production recombinant proteins with kinase activity, used to develop drugs to treat cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 WIIGRRRGCDLSFPSNKLVSGDHCRIVVDEKSGQVTLEDTSTSGTVINKLKVVKKQTCPL 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 WIFGRNPACDYHLGNISRLSNKHFQIL--XXXXXXLLNDISTNGTWLNGQKVEKNSNQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 85; DB 4; Length 664
Pred. No. 0.025;
6; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cell cycle regulatory factor Cds1 SEQ ID NO:1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 34.8 Matches 23; Conservative
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Length 288;

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Query Match Local

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Matches

AAG89798;

AAG89798

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4 GRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine; tuberculosis; non specific adjuvant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campos-Neto A, Houghton R;
                    Query Match 24.3%; Score 81.5; DB 4; Best Local Similarity 38.5%; Pred. No. 0.027; Matches 25; Conservative 11; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis antigen TbRa10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 100-101; 190pp; English
                                                                                                                                                                                                                                                                                                                               AAW32352 standard; protein; 148 AA.
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Vedvick TH, Twardzik DR;
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95US-00532136.
96US-00620280.
96US-00658800.
96US-00680573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigen; immunogen; vaccine; skin testing; M.tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
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Best Local Similarity 28.8
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-192904/17.
                                                                                                                                                                                                                             273 VITVG 277
                                                                                                                                                                                     63 EITVG 67
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22-SEP-1995;
22-MAR-1996;
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12-JUL-1996;
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                                                                                                                                                                                                                                                 be used to detect inhibitors of cell cycle regulatory factors which can be applied in the development of drugs for treating cancers and proliferative diseases. Cds1 is strongly expressed in the testis as well as other tissues. Cds1 can efficiently phosphorylate cdc25 and histone H1
                                                                                                                                                                                                                             1 WTFGRNPACDY------HLGNISRLSNKHFQIL----XXXXXXLLNDISTNGTWLNG 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yokoi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                     14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; SEQ ID NO 3552; 246pp + Sequence Listing; English
                                                                                                                                           25.0%; Score 84; DB 3; Length 543; 29.1%; Pred. No. 0.027; ive 11; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ochiai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H, Ando S, Hayashi M,
Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C glutamicum protein fragment SEQ ID NO: 3552
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                           ELVGKGKRRPLNNNSEIAL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG89798 standard; protein; 288
                                                                                                                                                                                                                                                                                                          OKVEKNSNQLLSQGDEITV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99JP-00377484.
2000JP-00159162.
2000JP-00280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2000; 2000EP-00127688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                     23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mizoguchi F
Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-376931/40.
                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAH65017.
                                                                                                      Sequence 543 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-DEC-1999;
07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3P1108790-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUN-2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakagawa S,
Tateishi N,
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                                    immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, TBRaio. The immunogenic polypeptide can be used to diagnose M.tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----RLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
A new immunogenic polypeptide has been developed comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.7%; Score 79.5; DB 2; Length 148; 28.8%; Pred. No. 0.022; ive 16; Mismatches 15; Indels 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 GRNPACDYHLGNIS---
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Sequence 288 AA

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(CORI-) CORIXA CORP.
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nes 21; Conserv
                                                                                                                                                                                                                                                                                                          N-PSDB; AAV44340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 148 AA;
                                                                                                                                 Mycobacterium
                                                                                                                                                    WO9816645-A2
                                                                                                                                                                                           07-OCT-1997;
                                                                                                                                                                                                              11-OCT-1996;
13-MAR-1997;
                                                          17-OCT-2003
09-NOV-1998
                                                                                                                                                                        23-APR-1998
                                        AAW64292;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW81655
          AAW64292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence represents a M.tuberculosis antigen, TDRa10. The immunogenic protein, and fusion proteins containing one or more of the proteins pus ESAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against M.tuberculosis (for treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 GRHPDSDIFLDDVTVSRRHAEFRLENNEFNVV------DVGSLNGTYVNREPVD--- 113
 GRHPDSDIFLDDVTVSRRHAEFRLENNBFNVV------DVGSLNGTYVNREPVD--- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GRNPACDYHLGNIS------RLSNKHPQILXXXXXXLLNDI-STNGTWLNGQKVEKNS 54
                                                                                                                                                                                                                                                                                                                                                                                                                              New immunogenic polypeptide(s), from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also
                                                                                                                                                                      Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant; skin testing; M.tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 23.7%; Score 79.5; DB 2; Length 148; Best Local Similarity 28.8%; Pred. No. 0.022; Matches 21; Conservative 16; Mismatches 15; Indels 21;
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                                                                                                                                                                                                                                                                                                                                                                    Houghton
                                                                                                                                                                                                                                                                                                                                                                    Campos-Neto A,
                                                                                                                                                    Mycobacterium tuberculosis antigen TbRa10.
                                                                                         Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 94; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                   Dillon DC,
DR;
                                                                                       AAW32420 standard; protein; 148
                                                                                                                                                                                                                                                                                   95US-00523436.
95US-00533634.
96US-00620874.
96US-00659683.
                                                                                                                                                                                                                                                                 96WO-US014674
                                                                                                                                                                                                     Mycobacterium tuberculosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : :|: |||: :|
114 SAVLANGDEVQIG 126
                               ::|: |||::|
114 SAVLANGDEVQIG 126
                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
                   55 NOLLSOGDEITVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 NOLLSQGDEITVG
                                                                                                                                                                                                                                                                                                                                                                               Twardzik
                                                                                                                                                                                                                                                                                                                                                                    Skeiky YA,
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-192903/17.
                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT91465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 148 AA;
                                                                                                                                                                                                                         WO9709428-A2
                                                                                                                                                                                                                                                                 30-AUG-1996;
                                                                                                                                                                                                                                                                                    01-SEP-1995;
22-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                              Vedvick TH,
                                                                                                                                                                                                                                                                                                         22-MAR-1996;
                                                                                                                                                                                                                                                                                                                 05-JUN-1996;
                                                                                                                                                                                                                                              13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prevention)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis.
                                                                                                           AAW32420;
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                                                                    RESULT 25
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This polypeptide comprises Mycobacterium tuberculosis soluble antigen This polypeptide comprises Mycobacterium tuberculosis strain H37Rs expression library with rabbit anti-sera raised against M. tuberculosis supernatant. No significant homology was found between TDRa1 and Genebank database sequences. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAM64291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M-tuberculosis antigen, or an immunogenic portion of an M-tuberculosis antigen, as well as DNA sequences encoding such transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using the above detecting M. tuberculosis of infection in a patient using the above diagnosis of tuberculosis. (Updated on 17-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - used to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated Mycobacterium tuberculosis polypeptides and DNA - used develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campos-Neto A, Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.7%; Score 79.5; DB 2; Length 148; 28.8%; Pred. No. 0.022; Live 16; Mismatches 15; Indels 21
                                                                                                                                                                                                                                                                                                                          TbRa10.
                                                                                                                                                                                                                                                                                                                      Tuberculosis; infection; diagnosis; antigen;
                                                                                                                                                                                                                                                   Mycobacterium tuberculosis antigen TbRa10.
                                                                                                                                                                                                                                                                                                                                                                                                 tuberculosis; strain H37Ra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dillon DC, Ca
DR, Lodes MJ;
AAW64292 standard, protein; 148 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 99; 250pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-US018214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-00729622.
97US-00818111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reed SG, Skeiky YAW, Dill
Vedvick TS, Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAVLANGDEVQIG 126
                                                                                                                                   (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SS NOLLSQGDEITVG 67
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Houghton R;

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66 GRHPDSDIFLDDVTVSRRHAEFRLENVV------DVGSLNGTYVNREPVD--- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GRNPACDYHLGNIS-----RLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNS 54
                                                                                                                                                                                                                                                                                                                                            This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as current vaccination strategies do not provide 100% immunity
                                                                                                                                                                                                                                                                        New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen; immunotherapy; diagnosis; immunisation; vaccine; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.7%; Score 79.5; DB 2; Length 148; 28.8%; Pred. No. 0.022; ive 16; Mismatches 15; Indels 21
                                                                                                                                                             Campos-Neto A, Ho
J, Hendrickson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reed SG, Skeiky YAW, Dillon DC, Campos-Neto A, Ho
Vedvick TS, Twardzik DR, Lodes MJ, Hendrickson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M. tuberculosis antigen TbRalO amino acid sequence.
                                                                                                                                                                                Lodes MJ,
                                                                                                                                                                                                                                                                                                          Example 3; Page 136; 323pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY39094 standard; protein; 148 AA.
                                                                                                                                                             Dillon DC,
                                                                     98US-00024753
98US-00072596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-00025197
98US-00072967
                                     99WO-US003265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immune response; skin test.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : :|: |||: :|
114 SAVLANGDEVQIG 126
                                                                                                                                                                                Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 28.8 see 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 NQLLSQGDEITVG
                                                                                                                                                             Skeiky YAW,
                                                                                                                                                                                                                  WPI; 1999-527416/44.
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                                                                                                                           (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP
                                                                                                                                                                                                                                   N-PSDB; AAZ19038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 148 AA;
                                                                     18-FEB-1998;
05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9942076-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-MAY-1998;
                                     17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-NOV-1999
                                                                                                                                                                                Jedvick TS,
 26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY39094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 GRNPACDYHLGNIS------RLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis.
                                                                                                       Tuberculosis, immunogenic; soluble, antigen, protective immunity; TB; vaccine, pharmaceutical; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antigen; diagnosis; detection; infection; antibody; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                                                                    Houghton R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.7%; Score 79.5; DB 2; Length 148; 28.8%; Pred. No. 0.022; ive 16; Mismatches 15; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M. tuberculosis recombinant antigen protein TbRa10.
                                                                                                                                                                                                                                                                                                                                                                                                    Campos-Neto A,
                                                                   M. tuberculosis immunogenic polypeptide TbRal0
                                                                                                                                                                                                                                                                                                                                                                                                Dillon DC, Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 96; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY38957 standard; protein; 148 AA.
                                                                                                                                                                                                                                                                                                        96US-00730510.
97US-00818112.
                                                                                                                                                                                                                                                                      97WO-US018293
                                                                                                                                                           Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::|:|||:||
SAVLANGDEVQIG 126
                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOLLSQGDEITVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                Skeiky YAW,
3, Twardzik
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-261042/23.
                                                                                                                                                                                                                                                                                                                                                             (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAV64448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 148 AA;
                                                                                                                                                                                                                                                                  07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9942118-A2
                                                                                                                                                                                               WO9816646-A2
                                                                                                                                                                                                                                                                                                        11-OCT-1996;
                                                                                                                                                                                                                                                                                                                           13-MAR-1997;
                                 27-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                Reed SG, Sk
Vedvick TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-NOV-1999
                                                                                                                                                                                                                                   23-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY38957;
AAW81655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine;
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Matches
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AAY38957

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Houghton R;

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The present sequence represents a Mycobacterium tuberculosis protein. Products from the present invention, which describes protein fragments and nucleic acid fragments drow M.tuberculosis, can be used in the detection of and prevention of mycobacterial infections. In particular, the proteins and nucleic acids can be used for the diagnosis of or vaccination against tuberculosis caused by M. tuberculosis, M. africanum or M. bovis
                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of antigen CFP17.
                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 59; 265pp; English
                                                                                                                                                                                                                                                                                                                                      AAY21903 standard; protein; 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97DK-00001277.
98US-0070488P.
98WO-DK000132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-DK000438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (STAT-) STATENS SERUM INST.
                                                                                                                                                                                                                                                            ::|:|||::|
127 SAVLANGDEVQIG 139
                                                                                                                                                                                                                                                                                                                                                                                       06-SEP-1999 (first entry)
                                                                                                                                                  Local Similarity 28.8 nes 21, Conservative
                                                                                                                                                                                                                                            55 NQLLSQGDEITVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CFP25A; CFP30B; CFP7B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Andersen P, Skjot R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-347282/29.
N-PSDB; AAX81003.
                                                                                                               Sequence 161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09924577-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-NOV-1997;
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01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                AAY21903;
                                                                                                                                                                                                                   79
                                                                                                                                         Query Match
                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                        RESULT
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                                                                                The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's. M. tuberculosis Ag's. M. tuberculosis Ag's. DNa encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T, B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAZ1929 to AAZ192460 and AAX19083 to AAX19225 are used in the exemplification of
                                                                                                                                                                                                                                                                                                                                      GRNPACDYHLGNIS-----RLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis; antigen; vaccine; immunological; immunogen;
                      New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions.
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated mycobacteria polypeptides and nucleic acids - used developing products for the diagnosis of or vaccination against mycobacterial infections, particularly tuberculosis.
                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                    23.7%; Score 79.5; DB 2; Length 148; 28.8%; Pred. No. 0.022; ive 16; Mismatches 15; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosenkrands I, Weldingh K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis antigen CFP17.
                                                           Example 3; Page 96-97; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 127-128; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW72886 standard; protein; 161 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0044624P.
97DK-00001277.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (STAT-) STATENS SERUM INST.
                                                                                                                                                                                                                                                                                                                                                                                         SAVLANGDEVQIG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                           55 NQLLSQGDEITVG 67
                                                                                                                                                                                                                                                                                                 Conservative
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Florio W;
                                                                                                                                                                                                                    the present invention
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAV63917.
                                                                                                                                                                                                                                              Sequence 148 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Andersen P,
Oettinger T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9844119-A1
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10-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection
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The invention describes a substantially pure immunogenic polypeptide fragment (I) from Mycobacterium tuberculosis that is able to evoke a protective immune response against infections by mycobacteria belonging to the tuberculosis complex. The invention provides a (1) fusion polypeptide comprising at least one polypeptide fragment (I) and at least one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell epitope from M. tuberculosis protein ESAT-6, or MPTS9 and a second different amino acid sequence from M. tuberculosis, and/or including a sequence which protects the first amino acid sequence from in vivo degradation or post-translational processing; (3) a nucleic acid fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 GRNPACDYHLGNIS-----RLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNS
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                                                                                                                                                                                                                                                     21;
Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New immunogenic fragment of Mycobacterium tuberculosis
23.7%; Score 79.5; DB 2;
28.8%; Pred. No. 0.024;
iive 16; Mismatches 15;
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are useful as pharmaccuticals, for diagnosis of and as antigens for vaccination against TB caused by Mycobacterium tuberculosis, africanum or bovis. The polypeptides are also useful for diagnosing ongoing or previous sensitization in an animal with bacteria belonging to the tuberculosis complex. The invention also describes the use of CFP7A or response in a mammal; use of CFP7B, CFP19 or MPT59-ESAT6 or a T-cell epitope of for the induction of a strong immune response in a mammal; use of CFP7B, CFP19 or MPT59-ESAT6 or a T-cell epitope of for diagnosis of B in a mammal by performing a DTH type skin test; use of CFP27, CFP30A, RDI-ORF2, RDI-ORF5, MPT59-ESAT6, ESAT6-MPT59, CFP10A, CFP19, CFP27, CFP30B, CFP27, CFP30B, CFP19, CFP27, CFP30B, CFP19, CFP27, CFP30B, CFP19, CFP27, CFP25A, CFP30B, CFP7B or a T-cell epitope of for the preparation of a nimmunological composition; and for the preparation of a subunit vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of the Mycobacterium tuberculosis (Mtb) strain H37Rv gene Rv1827 product, designated CP17. This is one of 31 immunodominant secreted or cytosolic Mtb proteins of strain H37Rv (see AAM50729-59) discovered through the use of 2-dimensional liquid phase electrophoresis coupled with an in vitro interferon-gamma assay and liquid chromatography-mass spectrometry. The immunogens stimulate a strong interferon-gamma response from T cells of M. tuberculosis infected mice. The invention provides vaccine compositions for boosting immunity to mycobacteria when administered in mid-life to a subject who has been vaccinated neonatally or in early childhood with BCG and in whom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 GRHPDSDIFLDDVIVSRRHAEFRLENNBFNVV-----DVGSLNGIYVNREPVD--- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                       54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   life in a subject who has been vaccinated in childhood with Bacillus
Calmette-Guerrin, has purified proteins from mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine for boosting immunity to mycobacteria when administered in mid-
  The polypeptides and nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                     GRNPACDYHLGNIS------RLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNS
                                                                                                                                                                                                                                                                                                                                                                                            21;
                                                                                                                                                                                                                                                                                                                                                23.7%; Score 79.5; DB 2; Length 162;
28.8%; Pred. No. 0.024;
tive 16; Mismatches 15; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis immunodominant Mtb protein CP17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunogen; mycobacteria; immunisation; vaccine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (COLS ) UNIV COLORADO STATE RES FOUND.
  encodes the above polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM50735 standard; protein; 162 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Belisle JT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-164602/21.
                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 21; Conserv
                                                                                                                                                                                                                                                                                                          Sequence 162 AA;
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                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                          47
                                                                                                                                            4 GRNPACDYHLGNIS------RLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 WTFGRNPACDY------HLGNISRLSNKHFQIL-----XXXXXXLLNDISTNGTWLNG
                                                                                                                  21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides the protein and coding sequences of a human Chk2 phosphoenzyme inhibitor. The sequences can be used in the chemotherapy of cancers. The present sequence is the protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New gene encoding a protein for inhibiting human Chk2 phosphoenzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
                                                                                      23.7%; Score 79.5; DB 5; Length 162; 28.8%; Pred. No. 0.024; ive 16; Mismatches 15; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Human; Chk2 phosphoenzyme inhibitor; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.9%; Score 77; DB 5; 27.8%; Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 13-16; 36pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                     Human Chk2 phosphoenzyme inhibitor.
                                                                                                                                                                                                                                                                                        AAM48994 standard; protein; 514 AA.
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128 SAVLANGDEVQIG 140
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                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                       Query Match
Best Local Similarity 28.8
Matches 21; Conservative
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nes 22; Conserv
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                                                                Sequence 162 AA;
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Matches
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RESULT

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The present invention describes a method for detecting a cancer cell in a subject, which comprises determining the level of nucleic acid that is subject, which comprises determining the level of nucleic acid or map bosition 8q2.3 of the human genome or its expression product in a sample of the subject, where an elevated level of the concert in a subject comprising a cancer in the subject. Also described: (1) a method for diagnosing a cancer or predicting recurrence of a cancer in a subject comprising a cancer or predicting recurrence of a cancer in a subject complex; (2) the isolated or protein encoded by a nucleic acid as described above; (2) the isolated or complex; (3) a kit for detecting cancer cell; (3) an isolated or recombinant protein complex; (4) an antibody that binds to the protein complex; (5) a kit for detecting cancer cell; (3) an isolated or complex; (5) a kit for detecting or producin parting the protein complex; (5) a kit for detecting or producin danting the protein associated with DNA repair or damage, a nuclear targeting protein, and a second polypeptides selected from a protein having tumour suppressor activity, a protein having cell cycle modulatory activity, a protein associated with DNA repair or damage, a nuclear targeting protein, and a concound polypeptide is sufficient to bind to the EDD polypeptide or the EDD polypeptide or the EDD polypeptide or determining a modulator of the activity, formation or stability of an isolated or recombinant protein complex; (5) a method for determining a modulator of the activity, formation; (10) a method for treating a condition associated with celevated expression of EDD protein in a cell; (11) an antisense nucleic acid, ribozyme, PNA, interfering RNA or siRNA, inderfering RNA or siRNA, and cribozyme, PNA, interfering RNA or siRNA, independent or can be used in gene therapy. The methods and modulator are useful for treating a condition associated with EDD over expression such single acancer or can be used in gene therapy.
                                                                                                                                                                                                          detection; cancer; 8q22.3; chromosome 8; human; EDD; tumour suppressor; cell cycle modulator; DNA repair; DNA damage; nuclear targeting proteain; progesterome receptor; cytostatic; gene therapy; squamous cell carcinoma; hepatocellular carcinoma; ovarian cancer; breast cancer; melanoma; hepatocellular carcinoma; ovarian cancer; breast cancer; melanoma; gastrointestinal cancer; renal cell cancer; bladder cancer; prostate cancer; non-squamous carcinoma; gioblastoma; medullablastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting a cancer cell in a subject sample, also related to cancer treatments, comprises determining the level of nucleic acid that is linked to map position 8q22.3 of the human genome or its expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clancy J, Henshall S;
                                                                                                                                                                Human Chk2 transcript variant 2 protein SEQ ID NO:21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 29; SEQ ID NO 21; 331pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Henderson M,
P;
                      ADL32563 standard; protein; 514 AA
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                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                     variant 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Watts C, Saunders D,
Sutherland R, O'brien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-248472/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADL32562
                                                                                                                                                                                                                                                                                                                                                                                Chk2 transcript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004022750-A1
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                 03-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product
ADL32563
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e.g. squamous cell carcinoma, hepatocellular carcinoma, ovarian cancer, breast cancer, melanoma, head and neck cancer, adenocarcinoma, squamous lung cancer, gastrointestinal cancer (e.g. gastric, colon, or pancreatic cancer), renal cell cancer, bladder cancer, prostate cancer, non-squamous carcinoma, glioblastoma and medullablastoma. The components and composition are useful for reducing the expression of EDD in a cell to inhibit cellular proliferation. The present sequence represents human chk2 transcript variant 2 protein, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a number of peptides which disrupt the G2 cell cycle checkpoint when administered to a cell. They act by inhibiting Chk2 (the sequence of which is shown here) and Chk1 kinases, and may be derived from Cdc25C. The peptides are useful in the treatment of cell proliferation diseases, such as cancer, as the inhibition of the Chks allows DNA damage and induces apoptosis
                                                                                                                                                                                                                                                                        47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, Cdc25C; Chk1; Chk2; G2 checkpoint; cell cycle regulation; cancer; cell proliferation; apoptosis.
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                                                                                                                                                                                                                                                         1 WIFGRNPACDY-----HLGNISRLSNKHFQIL-----XXXXXXLLNDISTNGTWLNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated or recombinant polypeptide of 7-11 amino acids, useful for treating cell proliferative disorders, e.g. to stop the growth of, or kill cancer cells, by disrupting the G2 cell cycle arrest checkpoint.
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                                                                                                                                                                                              Length 514;
                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                           22.9%; Score 77; DB 8;
27.8%; Pred. No. 0.23;
tive 11; Mismatches 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 26; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Chk2 kinase protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                              Ź
                                                                                                                                                                                                                                                                                                                                                   173 ELVGKGKRRPLNNNSEIAL 191
                                                                                                                                                                                                                                                                                                                                                                                                                              AAG68375 standard; protein; 542
                                                                                                                                                                                                                                                                                                                     99
                                                                                                                                                                                                                                                                                                                      OKVEKNSNQLLSQGDEITV
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                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-343125/36.
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nes 22; Conserv
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nes 22; Conserv
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                                                                                                                                                                 Sequence 514 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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30-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG68375;
                                                                                                                                                                                                                                                                                                                     48
                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                Best Loc
Matches
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AAY05765;
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RESULT 37
          AAY05765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a novel human checkpoint kinase, termed hCDS1, that acts in coordination with Cdc25 in the DNA damage checkpoint. The sequence is predicted from a CDNA (see AAXS8793) isolated from a SK-N-MC neuroblastoma cDNA library. The predicted protein is 28% identical to the cdc1 protein of S. pombe. A 2.2 kb transcript is expressed in testis and in 8 human cancer samples examined. hCDS1, its inhibitors and activators, are useful for treating cancer or proliferative disease (claimed). Inhibitors and activators of the kinase activity can also be used in anti-cancer therapy, particularly by increasing susceptibility of cancer cells to chemotherapy and/or radiotherapy (claimed). hCDS1 is useful for modifying DNA damage checkpoint activity of a cancer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human kinase used for treatment of cancer and proliferative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 WIFGRNPACDY------HLGNISRLSNKHFQIL-----XXXXXXLLNDISTNGTWLNG 47
         WIFGRNPACDY-----HLGNISRLSNKHFQIL----XXXXXXXLLNDISTNGTWLNG 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                 Checkpoint kinase; hCDS1; human; DNA damage; proliferative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.9%; Score 77; DB 2; Length 543; 27.8%; Pred. No. 0.24; ive 11; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                              Blasina A;
                                                                                                                                                                                                                                                                                                                                                              Mcgowan C,
                                                                                                                    AAY06204 standard; protein; 543 AA
                                                                 172 ELVGKGKRRPLNNNSEIAL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELVGKGKRRPLNNNSEIAL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 OKVEKNSNOLLSOGDEITV 66
                                               99
                                                                                                                                                                             Human checkpoint kinase hCDS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Fig 2; 39pp; English.
                                               OKVEKNSNQLLSQGDEITV
                                                                                                                                                                                                                                                                                           98WO-EP006981.
                                                                                                                                                                                                                                                                                                            97GB-00022320.
                                                                                                                                                           (first entry)
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Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                              Luyten WHML, Parker AE,
                                                                                                                                                                                                                                                                                                                               (SCRI ) SCRIPPS RES INST
(JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-338010/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 543 AA;
                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAX58793
                                                                                                                                                                                                             cancer; therapy
                                                                                                                                                                                                                                                                                         21-OCT-1998;
                                                                                                                                                                                                                                                   WO9925843-A2
                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                             22-OCT-1997;
                                                                                                                                                           16-AUG-1999
                                                                                                                                                                                                                                                                      27-MAY-1999.
                            113
                                                                                                                                       AAY06204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (claimed)
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                                               48
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                                                                                                RESULT 36
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The present sequence represents hCDS1, a novel human cell cycle checkpoint kinase that acts in coordination with Cdc25 at the DNA damage checkpoint, rather than the replication checkpoint as found in yeast. The hCDS1 sequence was predicted from hCDS1 cDNA (see AAX25464) that was chost and a human SK-N-MC neuroblastoma cDNA library. It shows 28% cotained from a human SK-N-MC neuroblastoma cDNA library. It shows 28% cotained from a human SK-N-MC neuroblastoma cDNA library. It shows 28% cotained from a human SK-N-MC neuroblastoma cDNA library. It shows 28% cotained from a human SK-N-M neuroblastoma of N-S and 27% identify to the DWN kinase of S. cerevisiae. Northern blot analysis cidentified a single transcript of about 2.2 kb expressed in testis and in 8 human cancer samples examined. The characterisation of hCDS1 and the classifier of paramaceuticals and theraspeutic methods for acting as an adjunct to chemotherapy of cancer. Thus, pharmaceutical formulations cantibodies against the protein, or other therapeutics identified in caseasys of the invention, can be administered in conjunction with any suitable chemotherapy agent to act as an adjunct to the main action of the chemotherapy agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47
                                                                                                                                                                                                                              Ccell cycle checkpoint kinase; human; hCDS1; cell proliferation; cancer;
therapy; chemotherapy; adjunct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human cell cycle checkpoint kinase hCDS1, useful for treating cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proliferation diseases, e.g. cancer.
                                                                                                                                                                                       Novel human checkpoint kinase hCDS1
AAY05765 standard; protein; 543 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 33-34; 35pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-EP006982,
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                                                                                                                        (first entry)
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Best Local Similarity
Matches 22; Conserv
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                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                              WO9920747-A2
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                                                                                                                        02-AUG-1999
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AAM48996
ID AAM48
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AC AAM48
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Gaps

14;

47

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114 W-FGRDKSCEYCFDEPLLKRTDKYRTYSKKHFRIFREVGPKNSYIAYIEDHSGNGTFVNT 172
                                                                 The present invention provides the protein and coding sequences of a human Chkz phosphoenzyme inhibitor. The sequences can be used in the chemotherapy of cancers. The present sequence is a protein described in the exemplification of the invention
                                                                                                                                                                                           1 WIFGRNPACDY-----HLGNISRLSNKHFQIL-----XXXXXXLLNDISTNGTWLNG
          encoding a protein for inhibiting human Chk2 phosphoenzyme
                                                                                                                                                                                                                                                                                                                                                                                                               checkpoint kinase 2; CHK2; enzyme; antisense therapy
                                                                                                                                               Length 543;
                                                                                                                                                                    32; Indels
                                                                                                                                               22.9%; Score 77; DB 5; 27.8%; Pred. No. 0.24; iive 11; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                        Human checkpoint kinase 2 (CHK2) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 87-90; 100pp; English.
                                             Disclosure; Page 20-23; 36pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        represents the human CHK2 protein
                                                                                                                                                                                                                                                              ELVGKGKRRPLNNNSEIAL 191
                                                                                                                                                                                                                                                                                                                      ABG30701 standard; protein; 543
                                                                                                                                                                                                                                         OKVEKNSNQLLSQGDEITV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-DEC-2001; 2001WO-US048966.
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                                                                                                                                                                                                                                                                                                                                                                   07-OCT-2002 (first entry
                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sarthy A, Cowsert LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-575367/61.
N-PSDB; ABK88909.
                                                                                                                                             Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biological pathway
                                                                                                                           Sequence 543 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200251858-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-JUL-2002
           New gene activity.
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                                                                                                                                                                                                                                        48
                                                                                                                                                                                                                                                                                                                                                                                                                Human;
                                                                                                                                                                                                                                                                                                  RESULT 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of a human Chk2 phosphoenzyme inhibitor. The sequences can be used in the chemotherapy of cancers. The present sequence is a protein described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 WIFGRNPACDY-----HLGNISRLSNKHFQIL-----XXXXXXLLNDISTNGTWLNG
                                                                                                                                                                                                                                                    New gene encoding a protein for inhibiting human Chk2 phosphoenzyme activity.
                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                       22.9%; Score 77; DB 5; Length 543; 27.8%; Pred. No. 0.24; ive 11; Mismatches 32; Indels
                                Human Chk2 phosphoenzyme inhibitor related protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Chk2 phosphoenzyme inhibitor related protein #1.
                                                       Human; Chk2 phosphoenzyme inhibitor; cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; Chk2 phosphoenzyme inhibitor; cytostatic
                                                                                                                                                                                           (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK
                                                                                                                                                                                                                                                                                    Disclosure; Page 27-30; 36pp; Japanese
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                                                                                                                                               38-JUN-2000; 2000JP-00172273
                                                                                                                                                                     08-JUN-2000; 2000JP-00172273
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           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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N-PSDB; AAL44750.
                                                                                                                                                                                                                   2002-145186/19.
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les 22; Conserv
                                                                                                                                                                                                                             N-PSDB; AAL44751
                                                                                                                                                                                                                                                                                                                                                                   Sequence 543 AA;
                                                                                                   JP2001346588-A.
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                                                                              Homo sapiens
           08-JUL-2002
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                                                                                                                        18-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 39
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요
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The invention relates to an antisense compound targeted to a nucleic acid molecule encoding human checkpoint kinase 2 (CHK2). The antisense compound specifically hybridies with and inhibits the expression of human CHK2. The antisense compounds are useful as research reagents and diagnostics, in distinguishing between functions of various members of a biological pathway, and in the treatment of a disease or disorder, which can be treated by modulating the expression of CHK2. This sequence
New antisense oligonucleotides targeted to a nucleic acid encoding checkpoint kinase 2 (CHK2), useful for treating a disease or condition associated with CHK2, or in distinguishing functions of members of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 543 AA;
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Query Match 22.9%; Score 77; DB 5; Length 543; Best Local Similarity 27.8%; Pred. No. 0.24; Matches 22; Conservative 11; Mismatches 32; Indels
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Matches 22; Conservative 11; Mismatches 32; Indels 14; Gaps 3; Qy			
Matches	θ,	47	172
Matches	Gaps	GLMING	GTFVNT
Matches	14;	TSION	EDHSG
Matches	Indels	XXXXXX	: KNSYIAYI
Matches	32;		REVGE
Matches	Mismatches	NISRLSNKHFQII	 KYRTYSKKHFRIF
Matches	11;	HLG	LKRTD
Matches	Conservative	FGRNPACDY	FGRDKSCEYCFDEPL
Matches	22;	TW T	.14 W-
	Matches	δ	Db 1

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⁴⁸ QKVEKNSNQLLSQGDEITV 66 : | | : | : | : 173 ELVGKGKRRPLNNNSEIAL 191

Search completed: February 24, 2005, 15:19:39 Job time : 143.537 secs

us-09-936-956-19.rai

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GDELTVG 67
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US-09-300-008B-46
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Sequence 6, Appli
Sequence 18515, A
Sequence 1316, A
Sequence 1336, A
Sequence 1634, A
Sequence 1654, A
Sequence 16597, A
Sequence 16597, A
Sequence 17202, A
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                                                                                                                                            February 24, 2005, 15:14:52 ; Search time 33.7724 Seconds
(without alignments)
148.094 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17
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1 WTFGRNPACDYHLGNISRLS.....QKVEKNSNQLLSQGDEITVG
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(cgn2 6/ptodata1/iaa/5A_COMB.pep:*
(cgn2 6/ptodata1/iaa/5B_COMB.pep:*
(cgn2 6/ptodata1/iaa/6A_COMB.pep:*
(cgn2 6/ptodata1/iaa/6B_COMB.pep:*
(cgn2 6/ptodata1/iaa/BECOMB.pep:*
(cgn2 6/ptodata1/iaa/PCTUS_COMB.pep:*
(cgn2 6/ptodata1/iaa/backfiles1.pep:*
                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-198-46B-17
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US-08-198-46B-17
US-08-198-46B-6
US-08-198-46B-6
US-08-198-46B-6
US-09-248-796A-18515
US-09-902-540-1334
US-09-902-540-14917
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Maximum Match 100%
Listing first 45 summaries
                                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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ALIGNMENTS

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RESULT 1

US-03-100-008B-46

US-03-100-008B-16

US-03-100-008B-16

SEQUENCE 46, Application US/09300008B

PRACE No. 649534

SEQUENCE NO. 649534

TITLE OF INVENTION: A GENE ASSOCIATED WITH NIJMEGEN BREAKAGE

TITLE OF INVENTION: SYNDROME, ITS GENE PRODUCT AND METHODS FOR THEIR USE

TITLE OF INVENTION: SYNDROME, ITS GENE PRODUCT AND METHODS FOR THEIR USE

CURRENT PELLOR DATE: 1999-04-27

PRIOR PALLOR DATE: 1999-04-27

PRIOR PALLOR DATE: 1999-04-27

PRIOR APPLICATION NUMBER: US 60/083,269

PRIOR PALLOR DATE: 1999-04-27

NUMBER OF SEQ ID NOS: 64

SEQ ID NOS: 64

CORTANIAN: PASCHARIAN SACCHARIAN VERSION 3.0

SEQ ID NOS: 64

CORTANIAN: SACCHARIAN SACCHARIAN VERSION 3.0

SEQ ID NOS: 64

CORTANIAN: SACCHARIAN SACCH
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66 WTFGRNPACDYHLGNISRLSNRHFQILLGEDGNLLLNDISTNGTWLNGQRVERNSNQLLS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 WIFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hartwell, Leland H.
APPLICANT: Weinert, Ted A.
APPLICANT: Plon, Sharon E.
APPLICANT: Groudine, Mark T.
TITLE OF INVENTION: Cell Cycle Checkpoint Genes
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen O'Connor Johnson Kindness PLLC
STREET: 1420 Fifth Ave., Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/198,446B
FILING DATE: 18-FEB.1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Shainess, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: FHCR17537
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: 206-224-0779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 93.3%; Score 313.5; DB 2; 1 Similarity 89.7%; Pred. No. 2.2e-34; 61; Conservative 0; Mismatches 6;
FILING DATE: May 14, 1992
APPLICATION NUMBER: US 07/882,051
FILING DATE: Way 12, 1992
ATTORNEY AGENT INFORMATION:
NAME: Sheines, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: FHCR110798
TELECHONE: 206-682-8100
TELECHONE: 206-682-8100
TELECHONE: 206-682-8100
TELECHONE: 206-682-8100
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 176 amino acids
                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
DESCRIPTION: yeast MEC2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08198446B Patent No. 5674996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                         : 776 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  821 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
TOPOLOGY: linear
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126 QGDEITVG 133
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                                                                                                                                                                                                                                                                                                                                                            linear
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Best Local Similarity
Matches 61; Conserv
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                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-870-693-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 WTFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLS 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.3%; Score 313.5; DB 1; Length 776; 89.7%; Pred. No. 2.2e-34; Live 0; Mismatches 6; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/08870693

Patent No. 5866338

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Hartwell, Leland H.

APPLICANT: Plon, Sharon B.

APPLICANT: Plon, Sharon B.

TITLE OF INVENTION: Cell Cycle Checkpoint Genes

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Christensen O'Connor Johnson Kindness PLLC

STREET: 1420 Fifth Ave., Suite 2800
                                             COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/198,446B
FILING DATE: 18-FEB-1994
CLASSIFICATION: 536
ATTONEY/AGENT INFORMATION:
NAME: Sheiness, Diama K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: 35,356
REPRENCE/DOCKET NUMBER: 206-224-0779
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000
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COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,446
FILING DATE: PEDVLARY 18, 1994
APPLICATION NUMBER: PCT/US93/04458
FILING DATE: May 12, 1993
APPLICATION NUMBER: US 07/884,426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
JESCRIPTION: yeast MEC2 protein
US-08-198-468-17
                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 206-224-0779
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 776 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||||||||
| GDEITVG 133
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Best Local Similarity
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US-08-870-693-17
          COUNTRY:
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1; Gaps

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GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT PELLING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
RIOR PLING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-13
                              66 WIFGRNPACDYHLGNISRLSNKHFQILLGEDGNLLLNDISTNGTWLNGQKVEKNSNQLLS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 WYFGRDPNSDLQVASSSKISNKHFQIWLNFNDKSLWIKDTSTNGTHLNNSRLVKGSNYLL 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: CONCANNO et al.
TITLE OF INVENTION: SYNDROME, ITS GENE PRODUCT AND METHODS FOR THEIR USE
FILE REFERENCE: 924-0003-228
FILE REFERENCE: 924-003-228
CURRENT APPLICATION NUMBER: US 60/083,269
PRIOR APPLICATION NUMBER: US 60/083,269
PRIOR APPLICATION NUMBER: US 60/083,269
PRIOR FILING DATE: 1999-04-27
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSEQ for Windows Version 3.0
     1 WIPGRNPACDYHLGNISRLSNKHFQI-LXXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 WIFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXL-LNDISTNGTWLNGQKVEKNSNQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 165; DB 4; Length 513;
Pred. No. 3.2e-14;
9; Mismatches 22; Indels
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41.8%; Score 140.5; DB 4;
Best Local Similarity 46.3%; Pred. No. 6e-12;
Matches 31; Conservative 13; Mismatches 20;
                                                                                                                                                                                                                                                                                    Sequence 18515, Application US/09248796A Patent No. 6747137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Schizosaccharomyces pombe US-09-300-008B-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 52.2%;
Matches 36; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Candida albicans
US-09-248-796A-18515
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                                                                                                           60 QGDEITVG 67
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LENGTH: 64
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                                                                                                                                                                                   1 WIFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLS
                                                                                                                                       Gaps
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                                                                                  DB 1; Length 821;
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89.7%; Pred. No. 2.3e-34;
live 0; Mismatches 6; Indels 1
                                                                             ch 93.3%; Score 313.5; DB 1; Length S Similarity 89.7%; Pred. No. 2.3e-34; 61; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Christensen O'Connor Johnson Kindness PLLC STREEF: 1420 Fifth Ave., Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CUUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,693
FLING DATE:
FLING DATE: BORING BATA:
APPLICATION NUMBER: US/08/198,446
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/466
FILING DATE: FEDENUARY 18, 1994
APPLICATION NUMBER: US/07/884,426
FILING DATE: May 12, 1993
APPLICATION NUMBER: US 07/884,426
FILING DATE: May 12, 1992
APPLICATION NUMBER: US 07/884,051
FILING DATE: May 12, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: 35,356
REFERENCE/DOCKET NUMBER: BC 026,82-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hartwell, Leland H.
APPLICANT: Weinert, Ted A.
APPLICANT: Weinert, Ted A.
APPLICANT: Blon, Sharon E.
APPLICANT: Groudine, Mark T.
TITLE OF INVENTION: Cell Cycle Checkpoint Genes
NUMBER OF SEQUENCES: 19
ADDRESSEE: Christensen O'Connor Johnson Kindn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
DESCRIPTION: yeast MEC2 protein
DESCRIPTION: yeast MEC2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08870693
Patent No. 5866338
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 821 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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Best Local Similarity
Matches 61; Conserva
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US-08-198-446B-6
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US-08-870-693-6
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                                                                             Query Match
Best Local (
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i Sequence 16334, Application US/09902540

i Patent No. 6833447

i GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof C.

TITLE OF INVENTION: Wyxococcus xanthus Genome Sequences and Uses Thereof C.

TILLE OF INVENTION: Wyxococcus xanthus Genome Sequences and Uses Thereof CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR PILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 16334
                                                                                                                                Sequence 13360, Application US/09902540
; Sequence 13360, Application US/09902540
; Patent No. 683347
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Goldman, Roger C.
; APPLICANT: Misgand, Roger C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myacoccue xanthus Genome Sequences and Uses Thereof
; TILE REFERENCE: 38-10(15849) B
; CURRENT APPLICATION NUMBER: 60/217,883
; PRIOR PILING DATE: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQGD 62
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28.1%; Score 94.5; DB 4; Length 595;
Best Local Similarity 35.4%; Pred. No. 0.00019;
Matches 23; Conservative 17; Mismatches 20; Indels E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

28.1%; Score 94.5; DB 4; Length 103;
Best Local Similarity 36.9%; Pred. No. 2.2e-05;
Matches 24; Conservative 13; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16334
                        |||| :|
GDEIRIG 64
61 GDEITVG 67
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EISMG 83
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88 RILIG 92
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Waycoccous xanthus Genome Sequences and Uses Thereof; FILE REFERENCE: 38-10(15849) B.
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR PILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 10544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 10597, Application US/09902540
; Sequence 10597, Application US/09902540
; Patent No. 683147
; GRNERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Missend, Rocorcus xanthus Genome Sequences and Uses Thereof;
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof;
; TITLE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 27.8*; Score 93.5; DB 4; Length 311; Best Local Similarity 30.9*; Pred. No. 0.00012; Matches 21; Conservative 15; Mismatches 27; Indels
RESULT 10
US-09-902-540-10544
; Sequence 10544, Application US/09902540
; Patent No. 6813447
; GRNERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-10597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Myxococcus xanthus US-09-902-540-10544
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Query Match
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; Patent No. 683347
; GENERAL INFORMATION:
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Hinkle, Gregory J.
    APPLICANT: Slater, Steven C.
    TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
    FILE REFERENCE: 38-10(15849)B
    CURRENT FILING DATE: 2001-07-10
    FRIOR FILING DATE: 2001-07-10
    FRIOR FILING DATE: 2000-07-10
    NUMBER OF SEQ ID NOS: 16825
    SEQ ID NO 14372
           Sequence 14917, Application US/09902540

Sequence 14917, Application US/09902540

Sequence 14917, Application US/09902540

Sequence 14917, Application US/09902540

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcue xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION WHERE: US/09/902,540

CURRENT FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR PELING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 14917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 25.9%; Score 87; DB 4; Length 476; Best Local Similarity 36.9%; Pred. No. 0.0015; Matches 24; Conservative 10; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 25.6%; Score 86; DB 4; Length 614; Similarity 34.8%; Pred. No. 0.0029; 24; Conservative 16; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Myxococcus xanthus
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98 KPTDQVYIG 106
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Best Local Similarity
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US-09-902-540-14372
US-09-902-540-14917
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ORGANISM:
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; Sequence 17202, Application US/09252991A ; Patent No. 6551795

US-09-252-991A-17202

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; Sequence 18516, Application US/09248796A; Patent No. 6747137; RENEAL INFORMATION: APPLICANT: Keith Weinstock et al TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17202
LENGTH: SS8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 TIGRGPDNDWVLPDPERLVSSRHCTILNRDGVYYLTDTSTNGVLLVNAGHRLRRGNSEPL 151
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Mycococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10 (15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT PILING DATE: 2000-07-10
RRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 10166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.4%; Score 85.5; DB 4; Length 558; 33.3%; Pred. No. 0.003; ive 13; Mismatches 30; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
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US-09-902-540-10166
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129 P--LRSGDLVKVG 139
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152 QDGETVRLG 160
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US-09-902-540-10166
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TUBERCULOSIS
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                                                                                                                  Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
VERVION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
VENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Campos S.
APPLICANT: Workick, Daniel R.
APPLICANT: Workick, Daniel R.
APPLICANT: 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 98.09-/024

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FLING DATE: 13-MAR-1997
ATTONEY/AGERT INFORMATION:
NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 31,392
REGISTRATION STOCKET NUMBER: 210121.411C6
TELEFONG: (206) 622-4900
TELEFAK: (406) 622-4900
TELEFAK: (406) 622-4900
TELEFAK: (406) 642-631
INFORMATION POR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                       3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 65, Application US/08818111; Patent No. 6338852; GENERAL INFORMATION:
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : :|: |||: :|
114 SAVLANGDEVQIG 126
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                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 6300 CCCCTY: Seattle STATE: Washington
                                                                                                                                                      APPLICANT: Vedvick, APPLICANT: Twardzik, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
US-08-818-112-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (4),(9)
CTHER INFORMATION: Identity of amino acid sequences at the above locations are unknous-09-248-796A-18516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16059, Application US/09902540
; Sequence 16059, Application US/09902540
; Patent No. 683347
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Glater, Steven C.
; APPLICANT: Wisepand, Roger C.
; APPLICANT: Wisepand, Roger C.
; TITLE OF INVENTION: Wyxococcus xanthus Genome Sequences and Uses Thereof
; TITLE OF INVENTION: Wyxococcus xanthus Genome Sequences and Uses Thereof
; TITLE OF INVENTION: Wyxococcus (SO)
; CURRENT APPLICATION NUMBER: 08/09/02,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR PRIOR DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 WIFGRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLSQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 FSFGRNDTCDCEIDD-DRLSKLHCVITKENDSIWLLDKSTNSCLVNNTSVGK-GNKVLLR 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 83; DB 4; Length 149;
Pred. No. 0.0013;
8; Mismatches 30; Indels
       FOR DIAGNOSTICS AND THERAPEUTICS
                               FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18516
LENGTH: 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-818-112-64
Sequence 64, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 37.5%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Myxococcus xanthus US-09-902-540-16059
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 33.3
Matches 22; Conservative
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       TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-902-540-16059
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TUBERCULOSIS
                                                                                                                                                                                                                                                  66 GRHPDSDIFLDDVTVSRRHAEFRLENNEFNVV------DVGSLNGTYVNREPVD--- 113
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                                                                                                                                                                              15; Indels 21; Gaps
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                                                                                                                               ; Score 79.5; DB 3; Length 148;
; Pred. No. 0.004;
16; Mismatches 15; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Jodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 65, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campos-Neto, Antonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 65:
                                                                                                                                 Query Match 23.7%;
Best Local Similarity 28.8%;
Matches 21; Conservative 1
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114 SAVLANGDEVQIG 126
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LENGTH: 148 amino acids
LENGTH: 148 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 23.7%
Best Local Similarity 28.8%
Matches 21, Conservative
                                                                                                                                                                                                                                                                                                                  55 NOLLSQGDEITVG 67
                     TYPE: amino acid
STRANDEDNESS: single
; TOPOLOGY: linear
US-09-056-556-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 6300 Colum
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-072-596-65
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Patent No. 6350456

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Billon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.7%; Score 79.5; DB 3; Length 148; 28.8%; Pred. No. 0.004; Live 16; Mismatches 15; Indels 2:
                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FLING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION INFORMATION:
TELECHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556 FILING DATE: 07.APR-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 148 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 NOLLSQGDEITVG 67
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Matches 21; Conservative
                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 98104-7092
98104-7092
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US-09-056-556-64
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US-09-300-008B-43
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---DVGSLNGTYVNREPVD--- 113
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                                                                                                                                                                                                               APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Netc, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vewordick, Thomas S.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Hondrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.7%; Score 79.5; DB 4; Length 148; 28.8%; Pred. No. 0.004; tive 16; Mismatches 15; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKA, DAVId J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                   Sequence 64, Application US/09072967
Patent No. 6592877
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-050-739-6

Sequence 6, Application US/09050739
Patent No. 6641814
GENERAL INFORMATION:
APPLICANT: ANDERSEN, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : :|: |||: :|
114 SAVLANGDEVQIG 126
                           : : | : | | | : |
114 SAVLANGDEVQIG 126
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55 NOLLSOGDEITVG 67
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Best Local Similarity 28.8
Matches 21, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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Sequence 43, Application US/09300008B
; Sequence 43, Application US/09300008B
; Patent No. 645854
; GENERAL INFORMATION:
; APPLICANT: Concannon et al.
; TITLE OF INVENTION: A GENE ASSOCIATED WITH NIJMEGEN BREAKAGE
; TITLE OF INVENTION: SYNDROME, ITS GENE PRODUCT AND METHODS FOR THEIR USE
; TITLE OF INVENTION: BYSDROME, ITS GENE PRODUCT AND METHODS FOR THEIR USE
; CURRENT APPLICATION NUMBER: US/09/300,008B
; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: US 60/083,269
; RATOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 3.0
; LENGTH. AND 43
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APPLICANT: OFTINGER, Thomas
APPLICANT: MISSIN, TARAS
APPLICANT: RASWUSSEN, Peter Birk
APPLICANT: RASWUSSEN, Peter Birk
APPLICANT: RASWUSSEN, Peter Birk
APPLICANT: PLOINGH, Walter
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: NUMBER: U376/97
FILE REFERENCE: 670001-2002.1
CURRENT FILING DATE: 1999-03-10-10
EARLIER APPLICATION NUMBER: 60/044,624
EARLIER FILING DATE: 1997-04-18
EARLIER FILING DATE: 1997-04-18
EARLIER FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PATENTIN OF: 2.0
SOFTWARE: PATENTIN OF: 2.0
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; ORGANISM: Mycobacterium tuberculosis
US-09-050-739-6
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GENERAL INFORMATION:
APPLICANT: LUYTEN, Walter H.M.L.
APPLICANT: LUYTEN, Malter H.M.L.
APPLICANT: LUYTEN, Andrew E.
TITLE OF INVENTION: AND METHODS
TITLE OF INVENTION: AND METHODS
FILE REPERENCE: JAB 1333 (US)
CURRENT APPLICATION NUMBER: US/09/529,154
CURRENT APPLICATION NUMBER: PCT/EP98/06982
FRIOR APPLICATION NUMBER: PCT/EP98/06982
FRIOR APPLICATION NUMBER: PGB 9722320.0
FRIOR FILING DATE: 1998-10-21
FRIOR FILING DATE: 1997-10-22
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 2
LENGTH: 543
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Miagand, Roger C.
TITLE OF INVENTION: Mycococcus xanthus Genome Sequences and Uses Thereof FILE REPRENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
LENGTH: 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 22.9%; Score 77; DB 4; Length 543; Best Local Similarity 27.8%; Pred. No. 0.042; Matches 22; Conservative 11; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 10583, Application US/09902540; Patent No. 6833447
: | | : |: || : 173 ELVGKGKRRPLNNNSEIAL 191
                                                                                                                                                                         Sequence 2, Application US/09529154
Patent No. 6531312
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Matches 20; Conservative
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                                         US-09-949-016-10788

i Sequence 10788, Application US/09949016

j Patent No. 6812339

j GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYNORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TURERY APPLICATION NUMBER: US/09/949,016

CURRERY FILING DATE: 2000-04-14

PRIOR PLILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PLILING DATE: 2000-10-03

PRIOR PLING DATE: 20
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173 ELVGKGKRRPLNNNSEIAL 191
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Best Local Similarity 27.8°
Matches 22; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 22; Conserva
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ORGANISM: Human
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US-09-300-008B-45
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Miegand,
APPLICANT: Wiegand,
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(1549)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 15375
LENGTH: 640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 22.5%; Score 75.5; DB 4; Length 640; Best Local Similarity 31.8%; Pred. No. 0.083; Matches 21; Conservative 10; Mismatches 18; Indels 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09849617

GENERAL INFORMATION:

APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY

APPLICANT: GUO, Zijian

APPLICANT: GUO, Zijian

APPLICANT: GUO, Zijian

TITLE OF INVENTION: CHECKPOINT-ACTIVATING OLIGONUCLEOTIDES

FILE REFERENCE: CIT1350-1

CURRENT APPLICATION NUMBER: US/09/849,617

CURRENT FILING DATE: 2001-09-17

PRIOR APPLICATION NUMBER: US 60/202,028

PRIOR FILING DATE: 2000-05-04

NUMBER OF SEQ ID NOS: 14

SOCTAMARE: Patentin version 3.0

SEQ ID NO 2
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                                                                              US-09-902-540-15375; Sequence 15375, Application US/09902540; Patent No. 6833447; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 OKVEKNSNOLLSQGDEITV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT; ORGANISM: Myxococcus xanthus
US-09-902-540-15375
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Matches 20; Conservative
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GRGANISM: Xenopus laevis
US-09-849-617-2
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  106 KVELG 110
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                                                                                                          GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Miggand, Roger C.
TITLE OF INVENTION: Mycococcus xanthus Genome Sequences and Uses Thereof File Reference: 38-10 (15849) B.
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 15221
LENGTH: 200
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: U5/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR PLLING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 16276
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| :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| 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Patent No. 6458534
CENERAL INFORMATION:
APPLICANT: CONCENTION et al.
TITLE OF INVENTION: A GENE ASSOCIATED WITH NIJMEGEN BREAKAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 21.4%; Score 72; DB 4; Length 200; Best Local Similarity 33.3%; Pred. No. 0.061; Matches 22; Conservative 12; Mismatches 26; Indels
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Sequence 15221, Application US/09902540 Patent No. 6833447
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Matches 19; Conservative
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    Sequence 20980, Application US/09248796A
    Patent No. 6747137
    GENERAL INFORMATION:
    APPLICANT: Keith Weinstock et al
    APPLICANT: FILE OF INVENTION: UVCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
    TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
    FILE REFERENCE: 107196.132

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Patent No. 6727066
GENERAL INFORMATION:
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
CURRENT PELICATION 1002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR PILING DATE: 2000-07-28
NUMBER OF SEC ID NOS: 401
SOFTWARE: PERL PROGram
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                                                                                                                                                                                                                                                                                                                                                                                              Length 3256;
                                                                                                                                                                                                                                                                                                                                                                                                                                              28; Indels
                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
) OTHER INFORMATION: Incyte ID No. 6673549 2700132CD1
US-09-976-594-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEX: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 2700132CD1
US-09-919-039-21
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 19.9%; Score 67; DB 4;
Best Local Similarity 30.8%; Pred. No. 8.8;
Matches 20; Conservative 13; Mismatches 28
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PROL PROGRAM
SEQ ID NO 22
LENGTH: 3256
                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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US-09-248-796A-20980
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                                                                                                                                                                                                                TYPE: PRT
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Patent No. 6673549
Patent No. 673549
APPLICANT: Buchbinder, Jenny
APTLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS PILE REFERENCE: PA-0041 US
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TITLE OF INVENTION: SYNDROME, ITS GENE PRODUCT AND METHODS FOR THEIR USE FILE REFERENCE: 9924-0003-228
CURRENT PEPLICATION NUMBER: US/09/300,008B
CURRENT FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: US 6/083,269
PRIOR PILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FASTER OF FOR Windows Version 3.0
SEQ ID NO 45
                                                                                                                                                                                                                                                                                                                                                                                                                        ë
                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 64;
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                                                                                                                                                                                                                                                                                                                                                                ch 20.4%; Score 68.5; DB 4; Length 6 Similarity 34.4%; Pred. No. 0.047; 21; Conservative 9; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 2700132CD1
US-09-919-172-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 98, Application US/09919172

Patent No. 6673545

GENERAL INFORMATION:
APPLICANT: Faris, Mary
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA-0036 US
CURRENT APPLICATION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT APPLICATION NUMBER: 60/222,469

PRIOR APPLICATION NUMBER: 60/222,469

PRIOR PILLING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 102

SOFTWARE: PERL PROGRAM

SEQ ID NO 98

LENGTH: 3256
                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 30.8
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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US-09-976-594-22
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US-09-919-172-98
                                                                                                                                                                                                                                     LENGTH: 64
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; TYPE: PRT

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Sequence 41, Application US/09300008B

Sequence 41, Application US/09300008B

Batent No. 645834

GENERAL INFORMATION:

TITLE OF INVENTION: A GENE ASSOCIATED WITH NIJMEGEN BREAKAGE

TITLE OF INVENTION: SYNDROME, ITS GENE PRODUCT AND METHODS FOR THEIR USE

TITLE OF INVENTION: SYNDROME, US/09/300,008B

CURRENT APPLICATION NUMBER: US/09/300,008B

CURRENT APPLICATION NUMBER: US 60/083,269

PRIOR FILING DATE: 1998-04-27

NUMBER OF SEQ ID NOS: 64 0-27

SOFTWARE: PASICEQ for Windows Version 3.0

LENGTH: 64
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Sequence 42, Application US/09300008B

Batent No. 6458534

GENERAL INFORMATION:

APPLICANT: Concennon et al.

TITLE OF INVENTION: SYNDROME, ITS GENE PRODUCT AND METHODS FOR THEIR USE

TITLE OF INVENTION: SYNDROME, US/09/300,008B

CURRENT APPLICATION NUMBER: US/09/300,008B

CURRENT APPLICATION NUMBER: US/09/300,008B

NUMBER OF SEQ ID NOS: 64

NUMBER OF SEQ ID NOS: 64

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 63
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Best Local Similarity 27.5%; Pred. No. 2.9;
Matches 19; Conservative 16; Mismatches 23; Indels 11;
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CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
CENGTH: 883
                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-20980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 28.8
Matches 17; Conservative
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ORGANISM: Homo sapien
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                                                                                                                                                                                  APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REPERENCE: 3810(15849)B (CURRENT APPLICATION NUMBER: US/09/902,540 CURRENT FILING DATE: 2001-07-10 PRIOR FILING DATE: 2000-07-10 NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 12792
LENGTH: 177
TYPE: PRT
                                                                                                                                                        3 FGRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLSQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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19.0%; Score 64; DB 4; Length 177;
Best Local Similarity 34.5%; Pred. No. 0.66;
Matches 10; Conservative 8; Mismatches 11; Indels
                                                               Query Match 19.0%; Score 64; DB 4; Length 63; Best Local Similarity 32.8%; Pred. No. 0.19; Matches 21; Conservative 10; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 SMNGTWVNASSLGPDQDRMLNDGDALAFG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 SINGTWINGOKVEKNSNQLLSQGDEITVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: February 24, 2005, 15:25:31
Job time : 34.7724 secs
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12792, Application US/09902540 Patent No. 6833447 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Myxococcus xanthus
US-09-902-540-12792
ORGANISM: Homo sapien
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                     US-09-300-008B-42
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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 24, 2005, 15:23:51; Search time 96.9594 Seconds (without alignments)
226.127 Million cell updates/sec
Title: US-09-936-956-19
Perfect score: 336
Sequence: 1 WFGRNPACDYHLGNISRLS......QKVEKNSNQLLSQGDBITVG 67
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
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Total number of hits satisfying chosen parameters: 1380268 Minimum DB seq length: 0 Maximum DB seq length: 2000000000

1380268 seqs, 327241040 residues

Searched:

Maximum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Listing first 45 summaries

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUB_pep:*

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10: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 56, Appl	Sequence 11, Appl	Sequence 16, Appl	Sequence 7635, Ap	Sequence 10, Appl	Sequence 22674, A	Sequence 154547,	Sequence 2299, Ap	Sequence 809, App	Sequence 2, Appli	Sequence 1, Appli	Sequence 3552, Ap	Sequence 156334,
ΩI	US-10-857-622-56	US-09-740-627-11	US-10-081-119-16	US-10-032-585-7635	9 US-09-740-627-10	US-10-369-493-22674	US-10-424-599-154547	US-10-369-493-2299	US-09-764-864-809	US-09-780-525-2	US-09-740-627-1	US-09-738-626-3552	US-10-437-963-156334
DB	17	0	14	14	σ	15	15	15	σ	σ	9	σ	16
* Query Match Length DB ID	89	522	821	669	460	609	190	474	426	664	543	288	1141
% Query Match	93.3	93.3	93.3	50.0	40.9	27.7	26.5	25.7	25.3	25.3	25.0	24.3	23.8
Score	313.5	313.5	313.5	168	137.5	93	89	86.5	85	85	84	81.5	80
Result No.	٦	7	m	4	S	9	7	ω	6	10	11	12	13

8 14 US-10-193-002 8 15 US-094-194-3 2 16 US-10-620-246 2 16 US-10-32-112 3 14 US-10-185-185 3 15 US-10-185-185 3 15 US-10-185-185 3 15 US-10-424-599 9 10-09-740-627- 9 10-09-740-627- 9 10-09-740-627- 10 US-09-804-980 11 US-10-424-599 12 US-10-618-173 13 US-10-425-114 14 US-10-425-114 15 US-10-425-114 16 US-10-425-114 17 US-10-425-114 18 US-10-425-114 19 US-10-425-114 10 US-10-425-114 11 US-10-425-114 12 US-10-425-114 13 US-10-425-114 14 US-10-080-170 15 US-10-080-170 16 US-10-080-170 17 US-09-919-172-6 18 US-09-919-172-6 19 US-09-919-172-6 10 US-09-919-172-6 10 US-09-919-172-6		Sequence 6, Appli							Seguence	O)										233512 Sequence 233512,									74 Sequence 17	Sequence 9,	•
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4 US-10-193-002-65	US-09-791-171-6	.6 US-10-620-246-	.6 US-10-332-512A	.4 US-10-156-761-	.4 US-10-185-182A	.5 US-10-425-114-	US-09-738-626-5	.5 US-10-424-599-	US-09-740-627-9	.4 US-10-142-356-	-0 08-09-804-980-	.5 US-10-369-493-	US-09-849-617-2	.5 US-10-618-173-	US-09-738-626-3	.5 US-10-425-114-	.5 US-10-425-114-	.6 US-10-437-963-	.5 US-10-424-599-	4 US-10-156-761-	4 US-10-156-761-	.4 US-10-080-170-	.6 US-10-080-170-	.6 US-10-468-356-	US-09-764-864-1	US-09-919-172-9	.0 US-09-919-039-	.6 US-10-408-765A	.6 US-10-701-490-9	
	148 1	162	162	162	324	543	1082	143	229	459	545	162	513	517	517	154	617 1	228	1484 1	376	843 1	212	488	488	488	92	3256	3256 1	3256 1	3256 1	
8 6 6 7 7 7 8 8 9 7 7 7 8 8 9 7 7 7 8 8 9 7 7 7 8 8 9 7 7 7 9 9 9 9	23.7	23.7	23.7	23.7	23.2	22.9	22.9	22.8	22.8	22.8	22.3	22.2	22.0	21.9	21.9	21.7	20.8	20.5	20.5	20.4	20.4	20.5	20.1	20.1	20.1	19.9	19.9	19.9	19.9	19.9	
	79.5	79.5	79.5	79.5	78	77	77	76.5	76.5	76.5	75	74.5	74	73.5	73.5	73	70	69	69	68.5	68.5	68	67.5	67.5	67.5	67	67	67	67	67	

ALIGNMENTS

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RESULT 1
US-10-857-622-56
Sequence 56, Application US/10857622
Sequence 56, Application US/10857622
Sequence 56, Application US/10857622
Sequence 56, Application No. US20050026234A1
GENERAL INFORMATION:
APPLICANT: VIGLIA: JOHN ALEXANDRA
APPLICANT: VIGLIA: JOHN ALEXANDRA
APPLICANT: TSIEN, ROGER
APPLICANT: TSIEN, ROGER
APPLICANT: TSIEN, ROGER
APPLICANT: TSIEN, ROGER
APPLICANT: TSIEN, ROGER
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APPLICANT: TSIEN, ROGER
CURRENT APPLICATION NUMBER: US 09/865,291
PRIOR FILING DATE: 1090-00-13
PRIOR FILING DATE: 1090-00-13
PRIOR FILING DATE: 1090-00-13
PRIOR FILING DATE: 1090-01-31
SERIOR FILING DATE: 1090-01-31
SEQ ID NOS: 63
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Query Match 93.3%; Score 313.5; DB 17; Length 68; Best Local Similarity 89.7%; Pred. No. 7.7e-34; Matches 61; Conservative 0; Mismatches 6; Indels 1; Gaps

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Sequence 7635, Application US/10032585

Publication No. US20030180953A1

GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Command, Bussey
TITLE OF INVENTION Gene Disruption Methodologies for Drug Target Discovery
FILE REFREENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 7635
LENGTH: 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 WTFGRNPACDYHLGNISRLSNKHFQILLGEDGNLLLNDISTNGTWLNGQKVEKNSNQLLS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 WYPGRDPNSDLQVASSSRISNKHPQIWLNPNDKSLWIKDTSTNGTHLNNSRLVKGSNYLL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 WIFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXL-LNDISTNGTWLNGQKVEKNSNQLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 168; DB 14; Length 699;
Pred. No. 2.2e-13;
8; Mismatches 22; Indels
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Sequence 10, Application US/09740627

Patente No. USCOUL2964A1

GENERAL INFORMATION:

TITLE OF INVENTION: CELL CYCLE REGULATING FACTOR

FILE REFERENCE: 06501-071001

CURRENT FILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: US/09/740,627

PRIOR APPLICATION NUMBER: US/09/740,627

PRIOR APPLICATION NUMBER: US/09/740,627

PRIOR APPLICATION NUMBER: US/09/03350

PRIOR APPLICATION NUMBER: UP/1/192467

PRIOR FILING DATE: 1999-06-23

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10.
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; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-09-740-627-10
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Best Local Similarity 53.6%;
Matches 37; Conservative 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Candida albicans
US-10-032-585-7635
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122 NQGDEIAVG 130
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                                                                                                     126 QGDEITVG 133
                                                     60 QGDEITVG 67
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                             WIFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLS 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 522;
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Sequence 16, Application US/10081119

Publication No. US20030045491A1

Publication No. US20030045491A1

SAPLICANT: Reinhard, Christoph

APPLICANT: Chan, Vivien W.

TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic

TITLE OF INVENTION: TTK in Diagnosis and STREAMENTION: TARGET IN Cancer

FILE REPERENCE: 1632.002

CURRENT APPLICATION NUMBER: US/10/081,119

CURRENT FILING DATE: 2002-02-21

FRIOR RELIGHT OF UNDER: 2001-02-21

NUMBER: OF WINDOWN WINDER: 2001-02-21

NUMBER: PRESENCE: 1602-02-11

NUMBER: PRESENCE: 1602-02-11

NUMBER: PRESENCE: 1602-02-11

NUMBER: PRESENCE: 2001-02-21

SEQ ID NO: 38

SOFTWARE: FREUESC for Windows Version 4.0
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                                                                                                                                                                                                                                                                        Sequence 11, Application US/09740627
Patent No. US20020012964A1
GENERAL INFORMATION:
TITUE OF INVENTION: CELL CYCLE REGULATING FACTOR
FILE REFERENCE: 06501-071001
CURRENT APPLICATION NUMBER: US/09/740,627
CURRENT FILING DATE: 1099-06-23
PRIOR PILING DATE: 1999-06-23
PRIOR PILING DATE: 1999-06-23
PRIOR FILING DATE: 1999-06-23
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 93.3%;
Best Local Similarity 89.7%;
Matches 61; Conservative
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                                                                                                                                             OGDEITVG 68
                                                                                                     QGDEITVG 67
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Best Local Similarity
Matches 61; Conserva
                                                                                                                                                                                                                                RESULT 2
US-09-740-627-11
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LENGTH: 522
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Blater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(5205)B
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                          53 GRHPDCDLMLTHPS-ISRFHLQIRSNPSSRTFSLLDLSSVHGTWVSGRRIEPMVSVEMKE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 GRSNTCNYQLLQFT-ASYKHFRVYSVLIDDDMDFLVYCEDQSSNGTFLNHRLIGKGNSVL 136
                                                         4 GRNPACDYHLGNISRLSNKHFQIL---XXXXXXLLNDISTNGTWLNGQKVEKNSNQLLSQ
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; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REPREBRUCE: PT223
; CURRENT PAPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper; NUMBER OF SEQ ID NOS: 1792
; SEQ ID NO 809
; SEQ ID NO 809
; LENGTH: 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 25.7%; Score 86.5; DB 15; Length 474; Best Local Similarity 33.3%; Pred. No. 0.0094; Matches 23; Conservative 14; Mismatches 25; Indels 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: unsure

: LOCATION: (1)..(474)

: OTHER INFORMATION: unsure at all Xaa locations

US-10-369-493-2299
      Mismatches
                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 2299, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
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ORGANISM: Schizosaccharomyces pombe
      15;
      Conservative
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137 LSDGDILDV 145
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ORGANISM: Homo sapiens
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      Matches
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Sequence 154547, Application US/10424599

Bublication No. US20040031072A1

GENERAL INFORMATION:
GENERAL TA Rosa Thomas J

APPLICANT: La Rosa Thomas J

APPLICANT: Cov Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Soy Nucleic Acid Molecules and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 154547
                                                                                                                                                                                                                       APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TILLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)8
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 WRFGRHKSCEVVL-NGPRVSNFHFEIYQVYKIIVASXTRLVLIELQSLXDIIIXRNDPGH 118
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119 RNDSDESENVVFLHGKSKGLKNLLKSSASSTFSNNFRHSSNGTFLNFVSESLIRLQFTDV 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 27.7%; Score 93; DB 15; Length 609; Best Local Similarity 23.2%; Pred. No. 0.0017; Matches 33; Conservative 12; Mismatches 21; Indels
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US-10-424-599-154547
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Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: unsure

: LOCATION: (1)..(609)

: OTHER INFORMATION: unsure at all Xaa locations

US-10-369-493-22674
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Publication No. US20030233675A1
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32.8%;
119 NSRTILSNGDEIRIG 133
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ORGANISM: Glycine max
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Best Local Similarity
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US-09-738-626-3552
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                                                                                                                                             Query Match
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NAME/KEY: SITE
LOCATION: (415)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                             , LOCATION: (420)
, OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-809
                                                                                                                                                                                                                                            1 WIFGRNPACDYHLGNISRLSNKHFQIL - - XXXXXXLLNDISTNGTWLNGQKVEKNSNQLL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 WIFGRNPACDYHLGNISRLSNKHFQIL--XXXXXXLLNDISTNGTWLNGQKVEKNSNQLL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 WTIGRRRGCDLSFPSNKLVSGDHCRIVVDEKSGQVTLEDTSTSGTVINKLKVVKKQTCPL
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Pred. No. 0.022;
6; Mismatches 35; Indels
                                                                                                                                                           Score 85; DB 9; Length 426;
Pred. No. 0.013;
6; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sin-Bing Zhou
APPLICANT: Yuan Zhu
APPLICANT: Yuan Zhu
APPLICANT: Yuan Zhu
APPLICANT: Yiao Chaturvedi
APPLICANT: Xiaotong Li
TITILE OF INVENTION: FHARL, A NEW RING FINGER PROTEIN
FILE REFERENCE: GP-70668-C1
CURRENT APPLICATION NUMBER: US/09/780,525
CURRENT PILING DATE: 2001-02-09
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASELSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence I. Application US/09740627
Fatent No. US20020012964A1
GENERAL INFORMATION:
TITLE OF INVENTION: CELL CYCLE REGULATING FACTOR
TITLE OF INVENTION: CELL CYCLE REGULATING FACTOR
FILE REFERENCE: 06501-071001
CURRENT APPLICATION NUMBER: US/09/740,627
CURRENT FILING DATE: 1999-06-23
FRIOR PELING DATE: 1998-06-23
FRIOR FILING DATE: 1998-06-23
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 2, Application US/09780525; Patent No. US20020004223A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.3%;
34.8%;
                                                                                                                                                         ch 25.3%;
1 Similarity 34.8%;
23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 23; Conserva
                                                                                                                                                           Query Match
Best Local Similarity
Matches 23; Conserva
                                                                                                                                                                                                                                                                                                                                                              100 QTĠĎVÍ 105
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                                                                                                                                                                                                                                                                                                                         59 SQGDEI 64
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4 GRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQGD 62
                                                                                                                                                                                                                                                                                    1 WTFGRNPACDY------HLGNISRLSNKHFQIL-----XXXXXXLLNDISTNGTWLNG 47
                                                                                                                                                                                                                                     Gaps
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24.3%; Score 81.5; DB 9; Length 288;
Best Local Similarity 38.5%; Pred, No. 0.025;
Matches 25; Conservative 11; Mismatches 24; Indels
                                                                                                                                                                            25.0%; Score 84; DB 9; Length 543; 29.1%; Pred. No. 0.023; tiye 11; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFOGRATION:
APPLICANT: NAKAGAMA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: CCHIAI, KEIKO
APPLICANT: YOKCI, HARUHIKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, ANGERIO
APPLICANT: OZAKI, AKI
CURRENT FILING DATE: 1999-12-16
CURRENT FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 3552
LENGTH: 288
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
LENGTH: 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 156334, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3552, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                 173 ELVGKGKRRPLNNNSEIAL 191
                                                                                                                                                                                                                                                                                                                                                                                       48 OKVEKNSNQLLSQGDEITV 66
                                                                                                                                                                                                        Best Local Similarity 29.19
Matches 23; Conservative
                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        273 VİTVG 277
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US-10-437-963-156334
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66 GRHPDSDIFLDDVTVSRRHAEFRLENNEFNVV------DVGSLNGTYVNREPVD--- 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Twardzik, Daniel R.
Lodes, Michael J.
Hendrickenn, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 21;
                                                                                                                                                                                                                                                                                                                                                                       Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEME: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Peb-2002
CLASSIFICATION: <unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                   NAME: Maki, David J.

REGISTRATAION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 62-631
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                   Query Match
23.7%; Score 79.5; DB 14;
Best Local Similarity 28.8%; Pred. No. 0.021;
Matches 21; Conservative 16; Mismatches 15;
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REFERENCE/DOCKET NUMBER: 210121.411C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                   TOPOLOGY: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-10-193-002-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
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; Sequence 64, Application US/10084843
; Publication No. US20030143243A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELBFAX: (206) 682-0
INFORMATION FOR SEQ ID NO: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 355
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114 SAVLANGDEVQIG 126
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STATE: Washington
COUNTRY: USA
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                                                                                                     APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBNCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 FGRHPECHVLVDHPSVSRFHLEVRSRRRQRRITV-----TDLSSVHGTWISGRRIP 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.8%; Score 80; DB 16; Length 1141; 26.3%; Pred. No. 0.18; ive 16; Mismatches 20; Indels 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ATDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT4530_56010C.1.pep
US-10-437-963-156334
                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure
LOCATION: (1)..(1141)
OTHER INFORMATION: unsure at all Xaa locations
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APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-011-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  % Sequence 65, Application US/10193002; Publication No. US20030135026A1 GENERAL INFORMATION: Reed, Steven G.
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Vedvick, Thomas S.
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Lodes, Michael J.
                                                                   Boukharov, Andrey A.
Barbazuk, Brad
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STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 26.3%
....nes 20, Conservative
Zhou, Yihua
Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Oryza sativa
                                      APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ANDERSEN, FRIKE
APPLICANT: NELESEN, FRIKE
APPLICANT: OETTINGER, Thomas
APPLICANT: RASMUSERN, Peter Birk
APPLICANT: RASMUSERN, Peter Birk
APPLICANT: RASMUSERN, Ida
APPLICANT: REMEDINGH, Karin
APPLICANT: FLORIO, Walter
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1
CURRENT FILING DATE: 1998-03-30
FRIOR APPLICATION NUMBER: 03/6/97
FRIOR FILING DATE: 1997-04-02
FRIOR FILING DATE: 1997-04-02
FRIOR FILING DATE: 1997-04-18
FRIOR APPLICATION NUMBER: 60/044,624
FRIOR FILING DATE: 1997-04-18
FRIOR FILING DATE: 1997-04-18
FRIOR FILING DATE: 1997-04-18
FRIOR FILING DATE: 1997-04-18
FRIOR FILING DATE: 1997-04-18
FRIOR FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SCOFTWARE: PALCETIN VET. Z.0
                                                                                                                                                                                                                                                                                                   4 GRNPACDYHLGNIS-----RLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
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                                                                                                                                                                                                    ; Score 79.5; DB 14; Length 148;
; Pred. No. 0.021;
16; Mismatches 15; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.7%; Score 79.5; DB 9; Length 162; 28.8%; Pred. No. 0.024;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Mismatches
                                                                                                      TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 6, Application US/10620246
; Publication No. US20040115211A1
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 6, Application US/09791171; Patent No. US20020094336A1; GENERAL INFORMATION:
                                                                                                                                                                                                  Query Match
Best Local Similarity 28.8%;
Matches 21; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAVLANGDEVQIG 140
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114 SAVLANGDEVQIG 126
                                                                                                                                                                                                                                                                                                                                                                                                 55 NOLLSOGDEITVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 NQLLSQGDEITVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Conservative
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Best Local Similarity
                                                                                                                                                      US-10-084-843-64
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Sequence 7, Application US/10332512A
Publication No. US20040180056A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICANT: ORME, Ian M.
APPLICANT: ORME, IAN M.
TITLE OF INVENTION: MID-LIFE VACCINE AND METHODS FOR BOOSTING ANTI-MYCOBACTERIAL IMMU
TITLE OF INVENTION: MUMBER: US/10/332,512A
CURRENT APPLICATION NUMBER: US/10/332,512A
CURRENT PEDICATION NUMBER: DCT/US01/21717
PRIOR APPLICATION NUMBER: US 60/217,646
PRIOR APPLICATION NUMBER: US 60/217,646
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Version 3.1
SSEQ ID NO 7
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APPLICANT: ANDERSEN, PEECE
APPLICANT: ANDERSEN, Rikke
APPLICANT: OFFILIGEN, PEECE
APPLICANT: OFFILIGEN, PEECE
APPLICANT: OFFILIGEN, PEECE
APPLICANT: OFFILIGEN, PEECE
APPLICANT: PASSENKENDS, Ida
APPLICANT: PROSENKENDS, Ida
APPLICANT: FLORIO, Walter
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
TITLE OF INVENTION: NUMBER: US/10/620,246
CURRENT APPLICATION NUMBER: 09/050,739
PRIOR FILING DATE: 1997-04-02
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR FILING DATE: 1997-01-18
PRIOR FILING DATE: 1997-01-18
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1999-10-2
PRIOR APPLICATION NUMBER: 60/116,673
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-10-08
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PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 21; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-620-246-6
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128 SAVLANGDEVQIG 140
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Best Local Similarity 28.89
Matches 21, Conservative
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PRIOR APPLICATION NUMBER: PCT/EP98/06981
PRIOR FILING DATE: 1998-10-21
PRIOR FILING DATE: 1997-10-22
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 543
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Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIRO
APPLICANT: HANDI, SEIRO
APPLICANT: HEROSHI
APPLICANT: HANDI, KEIRO
CHIAI, KEIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 ELVGKGKRRPLNNNSEIAL 191
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Best Local Similarity 31.0%,
Thes 22, Conservative
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                                                                                                                                                                                                                    ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-425-114-56100
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US-09-738-626-5092
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                                                                                                                                                                                                                            80 GRHPDSDIFLDDVIVSRRHAEFRLENNEFNVV-----DVGSLNGIYVNREPVD--- 127
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                                                                                                                                                                                              4 GRNPACDYHLGNIS-----RLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TFGRNPACDYHLGNISRLSNKHFQILXXXXXXL-LNDI-STNGTWLNGQKVEKNSNQLLS 59
                                                                                                23.7%; Score 79.5; DB 16; Length 162; 28.8%; Pred. No. 0.024; Live 16; Mismatches 15; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.2%; Score 78; DB 14; Length 324; 29.4%; Pred. No. 0.082; Live 19; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10185182A
Publication No. US2030017160A1
GENERAL INFORMATION:
APPLICANT: LUTTEN, Walter H.M.L.
APPLICANT: MACGOWAN, Clare H.
APPLICANT: MACGOWAN, Clare H.
APPLICANT: MACGOWAN, Alessandra
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: COMPOSITIONS AND METHODS
FILE REFERENCE: TSR 649.0 Div.1
CURRENT APPLICATION NUMBER: US/10/185,182A
CURRENT FILING DATE: 2002-09-04
PRIOR FILING DATE: 2002-09-04
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ONURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: BHIRAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHAKAKI, YOSHIUWKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFRERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-08-02
NUMBER: OF SEQ ID NOS: 15109
SEQ ID NO 14509
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 14509, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
                             ; ORGANISM: Mycobacterium tuberculosis
US-10-332-512A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-14509
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 29.48
Matches 20; Conservative
                                                                                                                         Best Local Similarity 28.8
Matches 21, Conservative
                                                                                                                                                                                                                                                                                          55 NQLLSQGDEITVG 67
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304 NGDEVQIG 311
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                                                                                                       Query Match
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Sequence 56100, Application US/10425114

Sequence 56100, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Pabaska, Jack E

APPLICANT: Pabaska, Jack E

APPLICANT: Pabaska, Jack E

APPLICANT: APPLICANT: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERENCE: 38-21(5313) B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 56100

LENGTH: 1082
                                                                                                                                                                            4 GRNPACDYHL-----GNISRLSNKHFQILXXXXXXLLNDISTNGTWL-NGQKVEKNSNQ 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GSNRSCNFPLNDQTISGNLCKI--KHTQ-GDGSAVAVLESMGSKGSVLVNGTHVKKNTSC 58
                                                                                                                                    1 WIFGRNPACDY-----HLGNISRLSNKHFQIL-----XXXXXXLLNDISTNGTWLNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.9%; Score 77; DB 15; Length 1082; 31.0%; Pred. No. 0.44; tive 16; Mismatches 23; Indels 10
Query Match 22.9%; Score 77; DB 14; Length 543; Best Local Similarity 27.8%; Pred. No. 0.2; Matches 22; Conservative 11; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: JC-GMLE01810018D04_FLI.pep
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1 WTFGRNPACDYHL-----GNISRLSNKHFQILXXXXXXLLN----DISTNGTWLNGQ 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 75; DB 14; Length 545;
Pred. No. 0.37;
9; Mismatches 33; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.8%; Score 76.5; DB 9; Length 459;
30.8%; Pred. No. 0.19;
tive 14; Mismatches 27; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BOYLEN, John F.
APPLICANT: Bowers, Alex J.
TITLE OF INVENTION: Serine-Threonine Kinase Member, h2520-40
FITHE REFERENCE: 010/1/31/77A
CURRENT APPLICATION NUMBER: US/10/142,356
CURRENT PILING DATE: 2002-05-09
PRIOR APPLICATION NUMBER: 60/290,276
PRIOR APPLICATION NUMBER: 60/290,276
PRIOR APPLICATION NUMBER: 60/290,276
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 545
TYPE: PRT
                                                                                                     Sequence 9, Application US/09740627

Patent No. US20020012964A1

GENERAL INFORMATION:

APPLICANT: Nakanishi, Makoto

TITUE OF INVENTION: CELL CYCLE REGULATING FACTOR

FILE REFERENCE: 06501-071001

CURRENT APPLICATION WUMBER: US/09/740,627

CURRENT FILING DATE: 2000-12-19

PRIOR FILING DATE: 1999-06-23

PRIOR FILING DATE: 1999-06-23

PRIOR FILING DATE: 1998-06-23

NUMBER OF SEQ ID NOS: 11

SOUTHWARE: FASELSEQ FOR WINDOWS Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/10142356
Publication No. US20030036183A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 OKVEKNSNQLLSQGDEITV 66
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29.1%;
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Matches 24; Conservative
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Best Local Similarity 29.1
Matches 23; Conservative
  163 HVGDVIRFG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
US-10-142-356-6
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US-10-142-356-6
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                                                                                         US-09-740-627-9
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Publication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5223.8)
CURRENT APPLICANT: 2003-04-28

CURRENT FILING DATE: 2003-04-28

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

EDENGTH: 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 22.8%; Score 76.5; DB 9; Length 143; Best Local Similarity 31.3%; Pred. No. 0.051; Matches 21; Conservative 15; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_140086C.1.pep
US-10-424-599-187236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)..(229)
OTHER INFORMATION: unsure at all Xaa locations
                                                                             TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-03
SOFTWARE: PARENT: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin Ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5092
                     TATEISHI, NAOKO
SENOH, AKIHIRO
YOKOI, HARUHIKO
                                                                IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 SQGDEITVG 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GDEITVG 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM:
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85 YVFGRDKKCDYTFDIPVLNQTDRYKTYSKRHFRIFQELGHGHSRVANIEDLSGNGTFVNK 144
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                                                                                                                                                                                                                                                                                                                                                                                                       21.9%; Score 73.5; DB 9; Length 517; 25.3%; Pred. No. 0.55;
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Sequence 2, Application US/10618173

Sequence 2, Application No. US20040018603A1

GENERAL INFORMATION:

APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY

APPLICANT: GUO, Zijian

APPLICANT: DUNPHY, William

TITLE OF INVENTION: CHECKPOINT-ACTIVATING OLIGONUCLEOTIDES

FILE REFERENCE: CIT136-1

CURRENT APPLICATION NUMBER: US/10/618,173

CURRENT FILING DATE: 2003-07-11

PRIOR APPLICATION NUMBER: US 60/202,028

PRIOR APPLICATION NUMBER: US 60/202,028

PRIOR APPLICATION NUMBER: US 60/202,028

PRIOR SEQ ID NOS: 14

SOFTWARE: Patentin version 3.0

SEQ ID NO 2

LUMBER NO 2

LUMBER NO 2

SEQ ID NO 2
                   APPLICANT: GUO, Zijian
TITLE BEPLICANT: DUNPHY, William
TITLE OF INVENTY, WILLIAM
TILE REFERENCE: CIT1350-1
CURRENT APPLICATION NUMBER: US/09/849,617
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US 60/202,028
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APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 EIIGKGRTLPLTNNAËIAL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 EIIGKGRTLPLTNNAEIAL 163
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SOFTWARE: PatentIn version 3.0
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Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Xenopus laevis
                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Xenopus laevis
US-09-849-617-2
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Best Local Similarity
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10 (52052)8
FILE REFERENCE: 38-10 (52052)8
CURRENT PAPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
FIRMCTH: 613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 GRNPACDYHLGNIS------RLSNKHPQILXXXXXXLLNDI-STNGTWLNGQKVEKNS 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                22.2%; Score 74.5; DB 10;
28.8%; Pred. No. 0.11;
tive 15; Mismatches 16;
                                                                                       APPLICANT: Statens Serum Intitut
APPLICANT: Anderson, Peter
TITLE OF INVENTION: M. Tuberculosis Antigens
FILE REFERENCE: 670001-2002.4
CURRENT APPLICATION NUMBER: US/09/804,980
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 257
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 1578, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       ) ORGANISM: Mycobacterium tuberculosis
US-09-804-980-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
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Publication No. US20020086392A1
GENERAL INFORMATION:
                 Sequence 6, Application US/09804980; Publication No. US20030147897A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIVK-KDYILKNGDRIVFG 128
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Matches 23, Conservative
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Matches 21; Conserva
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US-10-369-493-1578
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US-09-804-980-6
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296 HWGEPAELAHGDIITLG 312
  55 ----NQLLSQGDEITVG 67
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FEATURE:
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Sequence 65407, Application US/10425114

Publication No. US20040034888A1

SEQUENCE 65407

SEMBRAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Screen, Steven E

APPLICANT: Screen, Steven E

APPLICANT: Cao, Yongwal

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NOS: 73128
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US-10-425-114-65407
                                                                                                                                                             APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR PILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
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PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Corynebacterium glutamicum
MIZOGUCHI, HIROSHI
                                                                                               YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                              HAYASHI, MIKIRO
OCHIAI, KEIKO
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ORGANISM: Zea mays
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APPLICANT:
APPLICANT:
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APPLICANT: Ear Rosa, Thomas J.
APPLICANT: Ear Rosa, Thomas J.
APPLICANT: Ear Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Burbazuk, Brad
APPLICANT: Burbazuk, Brad
APPLICANT: Burbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Saciose Mith
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 204966
SEQ ID NOS: 204966
SEQ ID NO 163118
                                                                                                                                         APPLICANT: Zhou, Yihuua APPLICANT: Zhou, Yihuua APPLICANT: Zhou, Yihuua APPLICANT: Zhou, Yihuua APPLICANT: Kovalic, David K. APPLICANT: Screen, Steven E APPLICANT: Cao, Yongwei TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313) B CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NO 56757 LENGTH: 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 TFGRNPACDYHLGNISRLSNKHFQIL---XXXXXXLLNDISTNGTWLNGQKV-EKNSNQL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 20.5%; Score 69; DB 15; Length 228; Best Local Similarity 36.4%; Pred. No. 0.86; Matches 28; Conservative 8; Mismatches 29; Indels 3
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US-10-425-114-56757
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US-10-437-963-163818
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Sequence 56757, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 HWGEPAELAHGDIITLG 219
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ORGANISM: Oryza sativa
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Sequence 4, Application US/10080170

Sequence 4, Application US/10080170

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
TITLE OF INVENTION: US/10/080,170
TITLE OF INVENTION: US/10/080,170
CURRENT APPLICATION NUMBER: US/10/080,170
PRIOR PILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652
SOFTHARE: PATENTIN VEY: 2.1
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                                                                                                                                    4 GRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVBKNSNQLLSQGD
                                                      S.
Query Match 20.4%; Score 68.5; DB 14; Length 843; Best Local Similarity 29.4%; Pred. No. 4.4; Matches 20; Conservative 16; Mismatches 27; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 20.2%; Score 68; DB 14; Length 212; Best Local Similarity 30.8%; Pred. No. 1.1; Matches 20; Conservative 14; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI WASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9696
                                                                                                                                                                                                                                                                                                                                                                      Sequence 9696, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Streptomyces avermitilis
US-10-156-761-9696
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                                                                                                                                                                                                     60 QGDEITVG 67
                                                                                                                                                                                                                                                    77 PGSAVHLG 84
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                                                                                                                                                                                                                                                                                                                                                      JS-10-156-761-9696
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 233512
LENGTH: 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 WTFGRNPACDYHLGNISRLSN----KHFQILXXXXXXLLN-DISTNGTWLNGQKVEKNSN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.4%; Score 68.5; DB 15; Length 376; 26.4%; Pred. No. 1.8; tive 19; Mismatches 29; Indels 5.
                                 GRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDISTNGTWLNG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT3847_52888C.1.pep
US-10-424-599-233512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SHEAF, TADAYOSHI
APPLICANT: SAKAKT, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-02
PRIOR PILING DATE: 2001-06-03
PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13999
                                                                                                                                                                                                                                                                                                     ; Sequence 233512, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 13999, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OWURA, SATOSHI
; APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Streptomyces avermitilis US-10-156-761-13999
                                                              724 LLKFFEENKEMLLSFGDSV 742
                                                                                                                            48 -- OKVEKNSNOLLSQGDEI 64
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ISHIKAWA, JUN
HORIKAWA, HIROSHI
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209 CMLNSGDEVVFG 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Glycine max
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Matches 19; Conserva
                                                                                                                                                                                                                                                                                US-10-424-599-233512
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Indels

Length 488;

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4 GRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQGD
                     Query Match 20.1%; Score 67.5; DB 16; Best Local Similarity 32.3%; Pred. No. 3.2; Matches 21; Conservative 13; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: February 24, 2005, 15:42:02 Job time : 97.9594 secs
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TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR TITLE OF INVENTION: TERATHENT OF MYCOBACTERIASES
TITLE OF INVENTION: TERATHENT OF MYCOBACTERIASES
TITLE OF INVENTION: TERATHENT OF MYCOBACTERIASES
CURRENT APPLICATION NUMBER: US/10/080,170
CURRENT FILING DATE: 2002-06-10
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652
NUMBER OF SEQ ID NOS: 652
LENGTH, 488
                                                                                           3;
                                                                                                                                    TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENEOMICS AS A TOOL FOR TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENEOMICS AS A TOOL FOR TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR FILLE DEFERENCE: 05394.0019
FILLE REFERENCE: 05394.0019
CURRENT APPLICATION NUMBER: US/10/468,356
CURRENT FILING DATE: 2003-08-19
PRIOR FILING DATE: 2002-02-22
PRIOR FILING DATE: 2002-02-22
NUMBER OF SEQ ID NOS: 655
SOFTWARE: PATENTIN VET. 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 GRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQGD 62
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                                           Query Match 20.1%; Score 67.5; DB 14; Length 488; Best Local Similarity 32.3%; Pred. No. 3.2; Matches 21; Conservative 13; Mismatches 26; Indels 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 4, Application US/10468356; Publication No. US20040197896A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ; ORGANISM: Mycobacterium leprae US-10-468-356-4
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US-10-080-170-4
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Best Local Similarity
Matches 21; Conserv
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475 VIRLG 479
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LENGTH: 488
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JS-10-080-170-4
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-864-1109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 WIIGRRRGCDLSFPSNKLVSGDHCRIVVDEKSGOVTLEDIXTSGTVINKLKV 91
                                                                                                                                                                                                                                                                                              APPLICANT: Rosen et al.
TITLE OF INVENDITON: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT PILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTMARE: PatentIn Ver. 2.0
SEQ ID NO 1109
LENGTH: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
19.9%; Score 67; DB 9; Length 92;
Best Local Similarity 32.7%; Pred. No. 0.57;
Matches 17; Conservative 6; Mismatches 27; Indels
                                                                                                                                                                                                       ; Sequence 1109, Application US/09764864; Patent No. US20020132753A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                           475 VIRLG 479
63 EITVG 67
                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: SITE
                                                                                                                                                                              US-09-764-864-1109
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd. Copyright

- protein search, using sw model OM protein February 24, 2005, 15:12:40; Search time 26.1463 Seconds (without alignments) 246.555 Million cell updates/sec Run on:

US-09-936-956-19 336 Title: Perfect score:

1 WIFGRNPACDYHLGNISRLS.....QKVEKNSNQLLSQGDEITVG 67 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

1: pirl: * 2: pir2: * 3: pir3: * 4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		a			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
-	313.5	93.3	821	-	A39616	protein kinase RAD
7	137.5	40.9	460	4	S58882	protein kinase Cds
m	87	25.9	15	~	A96962	FHA-domain contain
4	86.5	25.7		(1)	T43420	probable protein k
ഗ	ĽΩ	25.4		7	F83634	hypothetical prote
9	81	24.1	952	7	T18837	hypothetical prote
7	80	23.8	399	~	AC3089	conserved hypothet
80	80	23.8	399	7	G98197	hypothetical prote
σı	79.5	23.7	162	7	D70721	hypothetical prote
10	78.5	23.4	1524	7	A96950	•~
11	78	23.2	1587	7	G86467	hypothetical prote
12	75.5	22.5	234	~	AF2214	hypothetical prote
13	74.5	22.2	162	~	T44758	hypothetical prote
14	74	22.0	513	-	S43941	
15	71.5	21.3	386	7	B71407	hypothetical prote
16	70	20.8	583	~	T02045	
17	69.5	20.7	157	~	S76488	hypothetical prote
18	69.5	20.7	445	7	AB2022	hypothetical prote
19	69.5	20.7	546	7	AE1899	adenylate cyclase
20	67.5	20.1	463	~	T10015	hypothetical prote
21	67.5	20.1	488	~	F86911	erved hyp
22	67	19.9	2897	7	B48666	
23	67	19.9	2938	7	T30249	
24	67	19.9	3256	~	A48666	cell proliferation
25	66.5	19.8	230	7	A83872	hypothetical prote
56	ď.	19.5	397	~	D83437	hypothetical prote
27	65	19.3	579	7	T37248	
28	9	19.3	598	7	T32166	hypothetical prote
53	64.5	19.2	527	~	B70700	hypothetical prote

FHA domain [import Fha domain (homolo	Nijmegen breakage	probable ABC trans	hypothetical prote	probable membrane	hypothetical prote	hypothetical prote	probable membrane	penicillin-binding	protein C18H9.1 [i	hypothetical prote	oxi3 intron 3 prot	hypothetical prote	hypothetical prote	probable membrane
E86579 H72046	T00393	D70986	T49879	D96904	T19167	T16191	S51457	875331	D88188	876973	QXBY33	C90657	C85508	S52706
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18.8 18.8	18.5	18.3	18.3	18.0	17.9	17.9	17.9	17.9	17.7	17.7	17.7	17.7	17.7	17.7
63	62	61.5	61.5	60.5	9	9	9	9	59.5	59.5	59.5	59.5	59.5	59.5

ALIGNMENTS

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protein kinase RAD53 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
NyAlternate names: protein P2588; protein YPL153c; SPK1 protein
C;Species: Saccharomyces cerevisiae
C;Daccession: A33616; S651645

A;Molecule type: DNA A;Residues: 1-821 <STE> A;Cross-references: UNIPROT:P22216; GB:M55623; NID:g172656; PIDN:AAA35070.1; PID:g172657 A; Experimental source: strain S288C

Rizheng, P.; Fay, D.S.; Burton, J.; Xiao, H.; Pinkham, J.L.; Stern, D.F.
Mol. Cell. Biol. 13, 5829-5842, 1993
A,Title: SPK1 is an essential S-phage-specific gene of Saccharomyces cerevisiae that enchance number: A54697; MUID:93361015; PMID:8355715

A; Contents: annotation R; Purnelle, B.; Coster, F.; Goffeau, A. submitted to the Protein Sequence Database, May 1996 **Reference number: S65154

A;Accession: S65164
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: 1 PNA
A;Cross-references: EMBL:273509; NID:g1370325; PIDN:CAA97858.1; PID:g1370326; GSPDB:GN001
A;Experimental source: strain S288C (AB972)
B;Experimental source: strain S288C (AB972)
B;Purnelle, B.; Comblez, S.; Coster, F.; Naveau, F.; Goffeau, A.
B;Purnelle, B.; Comblez, S.; Coster, March 1996
A;Description: The sequence of 55 kb on the left arm of yeast chromosome XVI identifies ogue to the human phosphotyrosyl phosphatase activator PTPA and a homologue to the plant A;Reference number: S69428

A;Accession: S69446

A; Molecule type: DNA A; Residues: 1-821 < PUW>

A, Cross-references: EMBL: X96770; NID: 91403537; PIDN: CAA65568.1; PID: 91403556

A)Gene: SGD:RAD53; SPK1; MEC2; SAD1; MIPS:YPL153c A,Cross-references: SGD:S0006074; MIPS:YPL153c A,Map position: 16L

A) Description: serine/threonine-specific protein kinase
A;Note: contains low activity as tyrosine-specific protein kinase
A;Note: contains low activity as tyrosine-specific protein kinase
A;Note: contains low activity specific protein kinase brockers
C;Superfamily: protein kinase control; nucleus; phosphotransferase; serine/threonine-speci
F;68-133/Domain: kinase interaction domain homology «KIH»
F;196-466/Domain: protein kinase homology «KIN»
F;204-213/Region: protein kinase APP-binding motif
F;207/Active site: Lys #status predicted

12:16:17

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Feb

Fri

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C; Accession: A96962
R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Bally, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos A; Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Crose-references: UNIPROT:097LQ0; GB:AE001437; PIDN:AAK78484.1; PID:g15023366; GSPDB:GN
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable protein kinase (EC 2.7.1.-) mekl - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:298596; PIDN:CAB11196.1; GSPDB:GN00066; SPDB:SPAC14C4.03
A;Experimental source: strain 972h-; cosmid c14C4
                                                                                                                                                                                                                                                                                                                     - Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 TIGRKDDNSIML-NEGYVSGHHARVYLRNNQYILEDLNSTNGTVLNGQKIK--SKAYIKS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TFGRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQ 60
                                                                                                                                                                                                                                                                                                                 FHA-domain containing secreted protein [imported] - Clostridium acetobutylic;
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 16-Aug-2004 C;Accession: T43420; T37688
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A;Experimental source: strain 972h(-)
K:Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood,
submitted to the EMBL Data Library, August 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 445;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 87; DB 2; Length 159
Pred. No. 0.001;
9; Mismatches 29; Indels
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A;Molecule type: DNA
A;Residues: 1-445 <DEV>
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A;Introns: 53/1; 231/2
C;Superfamily: protein kinase homology
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A;Molecule type: DNA
A;Residues: 1-445 <LYN>
                                                                                                                      119 NŚRTILSNGDEIRIG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 25.9%;
Best Local Similarity 37.3%;
Matches 25; Conservative
                                            67
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                                                NSNQLLSQGDEITVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 GDEIKIG 151
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Best Local Similarity
Matches 23; Conserv
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A;Gene: CAC0504
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A; Residues: 1-202,'I',204-237,'F',239-460 < WOO>
A; Residues: 1-202,'I',204-237,'F',239-460 < WOO>
A; Residues: 1-202,'I',204-237,'F',239-460 < WOO>
A; Residues: 1-202,'I',204-237,'F',239-460 < WOO>
A; Cross-references: Strain 1972h(-); cosmid C18B5
B; Lindsay, H.D.; Griffiths, D.J.F.; Edwards, R.J.; Christensen, P.U.; Murray, J.M.; Osma Genes Dev. 12, 382-395, 1998
A; Title: S-phase specific activation of Cds1 kinase defines a subpathway of the checkpoi A; Reference number: Z26084; MUID: 98119835; PMID: 9450932
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F; 62-133/Domain: protein kinase homology <KIN>
F; 153-181/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein kinase Cds1 (EC 2.7.1.-) [validated] - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Schizosaccharomyces powher C (1920 - 1937 #text_change 09-Jul-2004 C (1920 - 1947 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004 C;Accession: S58882; S71846; T41204; T52473 C;Accession: S58882; S71846; T41204; T52473 Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374, 817-819, 1995 NJ Nature 374,
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A;Cross-references: BMBL:AJ222869; NID:g2689196; PIDN:CAA11019.1; PID:g2689197
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    Score 313.5; DB 1; Length 821;
Pred. No. 4e-32;
0; Mismatches 6; Indels 1.
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A,Residues: 1-60,'G',62-202,'I',204-460 <MUR2>
A;Cross-references: EMBL:X85040; NID:g794146; PIDN:CAA59410.1;
R,Wood, V.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez,
submitted to the EMBL Data Library, July 1999
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A;Cross-references: UNIPROT:Q09170; EMBL:X85040; NID:g794146
R;Murakami, H.
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A;Introns: 86/3; 103/1; 113/3; 142/1; 228/3; 298/3; 368/2
C;Function:
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; Pred. No. 1e-09;
13; Mismatches 22;
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A;Molecule type: DNA
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93.3%;
ilarity 89.7%;
Conservative
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A;Accession: T41204
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A;Gene: SPBC18B5.11c; cds1
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                                        Similarity
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Query Match
Best Local S
Matches 61
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Conserved hypothetical protein Atu4335 [imported] - Agrobacterium tumefaciens (strain C5 C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Spacession: AC3089 [Size Accession: AC3089] [Size Accession: AC3089] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size AC308] [Size
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: G98137
R;Goodner, B:; Hinkle, G:; Gattung, S:; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2332-2338, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUD:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein AGR_L_1057 [imported] - Agrobacterium tumefaciens (strain C58, Cere
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D70721
hypothetical protein Rv1827 - Mycobacterium tuberculosis (strain H37RV)
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Best Local Similarity 26.7%; Pred. No. 0.02;
Matches 20; Conservative 16; Mismatches
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A;Molecule type: DNA
A;Residues: 1-399 <KUR>
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A, Residues: 1-399 < KUR>
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A, Gene: Atu4335
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A;Accession: T18837
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Grotus: preliminary; translated from GB/EMBL/DDBJ
A;Residus: 1-952 <WIL>
A;Residus: 1-952 <WIL>
A;Cross-references: UNIPROT:P46012; EMBL:Z35595; PIDN:CAA84636.1; GSPDB:GN00020; CESP:CGA;Experimental source: clone C01G6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: F83634
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, i. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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A;Accession: R83634
A;Status: preliminary
A;Molacule type: DNA
A;Residues: 1-497 <STO>
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A;Experimental source: strain PAO1
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                                       57
                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein PA0081 [imported] - Pseudomonas aeruginosa (strain PA01) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep_2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
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Pred. No. 0.042;
9; Mismatches 11; Indels
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A;Introns: 34/2; 61/2; 101/3; 195/1; 218/3; 845/3; 886/3
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GRNPACDYHLGNISRLSNKHFQILXXXXXXLLN-
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Best Local Similarity 41.2%;
Matches 14; Conservative
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A,Gene: CESP:C01G6.5
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ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C., C.A; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall, Rizzo, Rochey, T.; Rowley, D.; Sakano, B.; Li, Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, J. Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: G86467
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                   A;Residues: 1.1587 <STO>
A;Cross-references: UNIPROT:Q9C8N3; GB:AE005172; NID:g10092383; PIDN:AAG12790.1; GSPDB:Gi
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1587;
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; Pred. No. 0.18;
16; Mismatches
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R;Parkhill, J; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, October 1997
A;Reference number: Z22833
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143 QPI--ILKDGDRVRLG 156
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29.9%;
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A,Gene: alr3269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Age 550
DNA segregation ATP-ase FtsK/SpoIIIE (three ATPases), contains FHA domain [imported] - C. Species: Clostridium acetobutylicum
C. Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C. Accession: A96550
R. Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
A. Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A. Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
(286467
hypothetical protein F7P12.4 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: G86467
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
     C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: D70721
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Comnor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Atitle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MuID:98295987; PMID:9634230
A;Accession: D70721
A;Molecule type: DNA
A;Residues: 1-162 <COL>
                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q50606; GB:Z78020; GB:AL123456; NID:g3261625; PIDN:CAB01474. C;Genetics: strain H37Rv C;Genetics: A;Gene: Rv1827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: A96950
A;Status: preliminary
A;Olacule type: DNA
A;Residues: 1-1524 «KUR»
A;Cross-references: UNIPROT:Q97LZ2; GB:AE001437; PIDN:AAK78388.1; PID:g15023260; GSPDB:(A)
C;Genetics: A;Genetics: A;Genetics: A;Gene: CAC0408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRNPACDYHLGNIS-----RLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 WTFGRNPACDYHLGNISRLSNKHFQILXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.7%; Score 79.5; DB 2; Length 162;
28.8%; Pred. No. 0.0095;
ive 16; Mismatches 15; Indels 21; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : :|: |||: :|
128 SAVLANGDEVQIG 140
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Best Local Similarity 28.8
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22; Conservative
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171 EDDQINI 177
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Cispecies: Nostoc sp. PCC 7120
A;Note: Nostoc sp. etrain PCC 7120
C;Date: Nostoc sp. strain PCC 7120
C;Date: Nostoc sp. etrain PCC 7120
C;Date: Nostoc sp. etrain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AF2214
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-234 «KUR»
A;Cross-references: UNIPROT:Q8YS22; GB:BA000019; PIDN:BAB74968.1; PID:g17132364; GSPDB:G?
A;Experimental source: strain PCC 7120
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                                                                                                                                  91 WIGRDRHNGICTYDKLLSRHHAAIKYVENQGF-----LLIDFQSTNGSFVNGEPVY 142
                                                                                    4 GRNPACDYHLGNISRLSNKHFQ1--LXXXXXXLLNDIST-NGTWLNGQKVEKNSNQLLSQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein MLCB1788.36c [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 WIFGR---NPACDY-----HIGNISRLSNKHFQILXXXXXXLLNDISTNGTWLNGQKVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein alr3269 [imported] - Nostoc sp. (strain PCC 7120)
4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Match 22.5%; Score 75.5; DB 2; Length 234; Local Similarity 30.3%; Pred. No. 0.046; les 23; Conservative 12; Mismatches 22; Indels 19
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C,Date: 03. Aug-1998 #sequence_revision 03. Aug-1998 #text_change 09-Jul-2004
C,Accession: B1407
B1407
B1407
B1407
B2 Beata, M.; Bantoft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
B; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giel
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans
C; Chalwatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal
A;Accession: B71407
A;Accession: B71407
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A;Wolecule type: mRNA
A;Residuse: 1-583 × BRA-
A;Cross-references: UNIPROT:049973; EMBL:U81960; NID:g2735007; PIDN:AAB93832.1; PID:g273
A;Experimental source: strain B73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Cross-references: UNIPROT: 023305; GB: Z97336; NID: 92244788; PID: e326894; PID: 92244805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: T02045.
R;Braun, D.M.; Stone, J.M.; Walker, J.C.
Rshraun, D.M.; Stone, J.M.; Walkary, December 1996
A;Description: Multiple receptor-like protein kinases interact with the KI domain of
                                                                                                                                                                                                                                   ----RNLINVIDKSRNGTFINGN 110
                                                                                                                                                                       48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55
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C;Species: Zea mays (maize)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 PGSTIRVGRIVRGNEIAIKDAGISTKHLRIESDSGNWVIQDLGSSNGTLLNSNALDPETS
                                                                                                                                                                       2 TFGRNPACDYHLG------NISRLSNKHFQILXXXXXXLLN--DISTNGTWLNGQ
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                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; nucleic acid sequence not shown; translation not A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29; Indels 11;
                                                                                                   20;
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                                       DB 1; Length 513;
                                                                                                   Indels
                                   22.0%; Score 74; DB 1; Le 29.1%; Pred. No. 0.17; ive 14; Mismatches 22;
                                                                                                                                                                                                                                   57 TIGRSRSCDVILSEPDISTFHAEFHLLOMDVDNFQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
                                                                                                                                                                                                                                                                                                                                                     111 RLVK-KDYILKNGDRIVFG 128
                                                                                                                                                                                                                                                                                                           49 KVEKNSNQLLSQGDEITVG
                            Query Match
Best Local Similarity 29.1%
Matches 23; Conservative
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Best Local Similarity 27.8*
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: T02045
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A; Mesidues: 1-513 - KaBL>
A; Cross-references: EMBL: 274149; NID: 91431139; PIDN: CAA98668.1; PID: 91431140; GSPDB: GN00
A; Experimental source: strain $288C
A; Ebokkovic, J.; Salz, J.E.; Soler-Mira, A.; Garcia-Cantalejo, J.; Revuelta, J.L.; Jimine
submitted to the EMBL Data Library, February 1996
A; Reference number: $67406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin C; Superfamily: protein kinase DUN1; kinase interaction domain homology; protein kinase h C; Keywords: ATP; nucleus; phosphoprotein; phosphotransferase; serine/threonine-specific F; 58-128/Domain: kinase interaction domain homology «KIH»
F; 198-480/Domain: protein kinase homology «KIN»
F; 206-214/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:P39009; EMBL:L25548; NID:g435616; PIDN:AAA16324.1; PID:g4356
R;Ballesta, J.P.G.; Remacha, M.; Soler-Mira, A.; Jimenez, A.; Garcia-Cantalejo, J.M.; Bd
Bubmitted to the Protein Sequence Database, July 1996
A;Reference number: 867629
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Yeast 12, 1077-1084, 1996
A;Title: The sequence of a 20.3 kb DNA fragment from the left arm of Saccharomyces cerev
A;Reference number: S72094; MUID:97051597; PMID:8896274
A;Accession: S72106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein kinase DUNI (BC 2.7.1..) - yeast (Saccharomyces cerevisiae)
NyAlternate names: protein D2370; protein YDL101c
C;Species: Saccharomyces cerevision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S43941; S67643; $\overline{8}$67418; S72106
R;Zhou, Z.; Elledge, S.J.
Cell 75, 119-112-1127, 1993
A;Title: DUNI encodes a protein kinase that controls the DNA damage response in yeast.
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
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A,Residues: 1-513 <BOS>
A,Cross-references: BMBL:X95644; NID:g1199535; PIDN:CAA64912.1; PID:g1199548
                                                                                                                                                                                                                                                                                                                                                                                                                                               GRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQGD
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                                                                                                                                   EMBL: AL008609; PIDN: CAA15468.1
                                                                                                                                                                                                                                                                                                       Query Match 22.2%; Score 74.5; DB 2; Length 162; Best Local Similarity 29.2%; Pred. No. 0.042; Matches 19; Conservative 18; Mismatches 23; Indels
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A;Residues: 1-513 <SAI>
A;Accession: T44758
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Cross-references: MIPS:YDL101c; SGD:S0002259
                                                            A,Molecule type: DNA
A,Residues: 1-162 <PAR>
A,Cross-references: UNIPROT:032919,
A,Experimental source: cosmid B1788
C,Genetics:
A,Note: MLCB1788.36c
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136 EVQIG 140
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A;Residues: 1-513 <ZHO>
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C,Accession: AE1899
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A;Reference number: AB1807; WUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:P94184; GB:BA000019; PIDN:BAB72700.1; PID:g17130088; GSPDB:GAA;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                          adenylate cyclase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 FTIGRLPECNLYL-PPAGVSRKHAQLVKKADGKWIIEDLGSRNGTQVN-QSIVSHPRQ-L 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 WIFGRNPACDYHLGNISRLSNKHFQILXXXXXX-LLNDI-SINGTWLNGQKVEKNSNQLL 58
  38 GRDPSCQVVLDAMMYRMVSRRHAVVRPVASSVDSKFSWVLCDLNSANGTYLNGQRL--YG 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Species: Mycobacterium leprae
C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein MLB1770.15c - Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Cole, S.T.
eubmitted to the EMBL Data Library, August 1997
A;Reference number: Z16916
A;Accession: T10015
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A;Molecule type: DNA
A;Residues: 1-463 <COL>
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96 COELHAGDRISLG 108
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                                                        55 NOLLSQGDEITVG
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Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Residues: 1-546 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: AE1899
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Mypothetical protein alr1728 [imported] - Nostoc sp. (strain PCC 7120)

C,Species: Nostoc sp. PCC 7120

C,Species: Nostoc sp. exrain PCC 7120

C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C,Accession: AB2022

C,Accession: AB2022

NAKAZAKi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Pilamentous Nitrogen-fixing Cyanobacterium And A;Reference_number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein - Synechocystis sp. (strain PCC 6803)
hypothetical protein - Synechocystis sp. (strain PCC 6803)
S.Speciess Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74688
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: S76488
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-157 <KAN>
A;Residues: 1-157 <KAN>
A;Cross-references: UNIPROT:P74513; EMBL:D90915; GB:AB001339; NID:g1653604; PIDN:BAA1861
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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A;Experimental source: strain PCC 7120
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                                                                                                           2 TFGRNPACDYHLGNISRLSNKHFQIL---XXXXXXLLNDISTNGTWLNGQKVEKNS----
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                                                        12;
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; Pred. No. 0.18; 
15; Mismatches 27; Indels 13
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20.8%; Score 70; DB 2; Length 583; 36.4%; Pred. No. 0.64; ive 7; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: S74322; MUID:97061201; PMID:8905231
                                                                                                                                                                                                                                                              262 HWGEPAELAHGDIITLG 278
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Best Local Similarity 28.6%;
Matches 22; Conservative 1
                                                     28; Conservative
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Best Local Similarity
                   Best Local Similarity
Matches 28; Conserv
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A;Molecule type: DNA
A;Residues: 1-445 <KUR>
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  Query Match
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A;Accession: T30249
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2938 GSTA>
A;Cross-references: UNIPROT:Q61769; EMBL:X82786; NID:g1177527; PIDN:CAA58026.1; PID:g117
A;Experimental source: strain CBA; testis
C;Genetics
A;Gene: Ki-67
C;Keywords: cell cycle control; nucleus; tandem repeat
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R;Schlueter, C.; Duchrow, M.; Wohlenberg, C.; Becker, M.H.G.; Key, G.; Flad, H.D.; Gerde
J. Cell Biol. 123, S13-522, 1993
A;Title: The cell proliferation-associated antigen of antibody Ki-67: a very large, ubiq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-3256 < SCH>
A, Residues: 1-3256 < SCH>
A, Cross-references: UNIPROT: P46013; EMBL: X65550; NID: 9415818; PIDN: CAA46519.1; PID: 94158
C, Keywords: alternative splicing; cell cycle control; nucleus; tandem repeat
F;29-91/Domain: kinase interaction domain homology < KIH>
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R;Takami, H; Nakasone, K; Takaki, Y; Maeno, G; Sasaki, R; Masui, N; Fuji, F; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A83872
A;Accession: A83872
A;Accession: A83872
A;Accession: A83872
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A;Cross-references: UNIPROT:Q9KBZ7; GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BAB054
A;Experimental source: strain C-125
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C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Species: Bacillus halodurans
C.Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 FGRSIECDIRI-QLPVVSQRHCPIVVQEQEALLYNFSSTNPTQVNGVTIDEPVR--LRHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 FGRGIECDIRI-QLPVVSKQHCKIEIHEQEAILHNFSSTNPTQVNGSVIDEPVR--LKHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein BH1777 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 FGRNPACDYHLGNISRLSNKHFQILXXXXXXLL-NDISTNGTWLNGOKVEKNSNQLLSQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 FGRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQG
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                                                                                                                                                                                                                                                                                                                                                                     Query Match 19.9%; Score 67; DB 2; Length 2938; Best Local Similarity 32.3%; Pred. No. 9; Matches 21; Conservative 12; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 19.9%; Score 67; DB 2; Length 3256; Best Local Similarity 30.8%; Pred. No. 10; Matches 20; Conservative 13; Mismatches 28; Indels
l for cell cycle progression.
A,Reference number: Z20787, MUID:96431717, PMID:8834799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A48666; MUID: 94043435; PMID: 8227122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell proliferation antigen Ki-67, long form - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
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                      Cispecies: Mycobacterium leprae

Cipate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

Cipate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

Cipates: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

Ricole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho

Ray, M.A.; Rutherford, K.M.

Nature 409, 1007-1001, 2001

A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq

A;Atitle: Massive gene decay in the leprosy bacillus.

A;Reference number: A86909; MUID:21128732; PMID:11234002

A;Accession: F86511

A;Accession: Prebliminary

A;Residues: 1-488 <STO>
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Cell proliferation antigen Ki-67 - mouse
Cell proliferation antigen Ki-67 - mouse
C;Species 12-Oct-1999 #text_change 09-Jul-2004
C;Date: 22-Oct-1999 #aquence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30249
R;Starboroy, M: Gell, K:; Brundell, E.; Hoog, C.
J. Cell Sci. 109, 143-153, 1996
A;Title: The murine Ki-67 cell proliferation antigen accumulates in the nucleolar and he
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C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 15-Mar-2004
C;Accession: B4866
R;Schlueter, C.; Duchrow, M.; Wohlenberg, C.; Becker, M.H.G.; Key, G.; Flad, H.D.; Gerde J. Cell Biol. 123, 513-522, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: UNIPROT:Q9CDE4; GB:AL450380; NID:g13092432; PIDN:CAC29530.1; GSPDB:q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-2897 <SCH>
A;Cross-references: EMBL:X65551
C;Reywords: alternative splicing; cell cycle control; nucleus; tandem repeat
F;29-91/Domain: kinase interaction domain homology <KIH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGOKVEKNSNQLLSQGD
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conserved hypothetical protein ML0022 [imported] - Mycobacterium leprae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 19.9%; Score 67; DB 2; Length 2897; Best Local Similarity 30.8%; Pred. No. 8.9; Matches 20; Conservative 13; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A48666; MUID: 94043435; PMID: 8227122
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Best Local Similarity
Local 21; Conserve
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VIRLG 479
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A,Status: preliminary
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A;Cross-references: UNIPROT:P71590; GB:Z80233; GB:AL123456; NID:g3261645; PIDN:CAB02440.
A;Experimental source: strain H37Rv
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-598 <DUZ>
A;Cross-references: EMBL:AF022971; PIDN:AAC25839.1; GSPDB:GN00023; CESP:C31B8.8
A;Experimental source: strain Bristol N2; clone C31B8
456 FSSNRVYSYYESNIRQI-----FQMDSGFPKTLPSDLGFSVSGALRWINGHQI-----LM 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: B70700
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 FGRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI--STNGT--WLNGQKVEKNSNQLL 58
                                                                                                                                                                                                                                                                                      hypothetical protein C3188.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T3166
R;Du, Z.; Goela, D.; Harper, M.
submitted to the BML Data Library, September 1997
A;Description: The sequence of C. elegans cosmid C3188.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein Rv0020c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 19.3%; Score 65; DB 2; Length 598; Best Local Similarity 29.4%; Pred. No. 2.9; Matches 20; Conservative 11; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Introns: 49/1; 77/3; 154/1; 181/2; 479/3; 525/3; 563/1
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Matches 21; Conservative
                                                                                                                                                 506 SSGDEFAV 513
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                                                                                         59 SQGDEITV
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(Species: Peeudomonas aeruginosa
(CiSpecies: Peeudomonas aeruginosa
(CiSpecies: IS-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Ju1-2004
(CACCESSION: D83437
Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A.Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor, A.Accession: D83437
A.Accession: D83437
A.Accession: preliminary
A.Residues: 1-397 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q91360; GB:AE004594; GB:AE004091; NID:g9947630; PIDN:AAG0505
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA1665
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Oa Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37248
R;Wada, K.; Sato, H.; Kinoh, H.; Kajita, M.; Yamamoto, H.; Seiki, M.
Gene 211, 57-62, 1998
A;Title: Cloning of three Caenorhabditis elegans genes potentially encoding novel matrix
A;Reference number: Z21645; MUID:98241501; PMID:9573338
A;Accession: T37248
A;Accession: T37248
A;Accession: preliminary; translated from GB/EMBL/DDBJ
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A;Experimental source: strain N2; mixed developmental stage
C;Keywords: hydrolase; metalloproteinase
                                                                                                                                                    4;
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                                                                                                                                                                                                            1 WTFGR-----NPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNS 54
                                                                                                                                                                                                                                              TFGRNPA-----CDYHLGNISR-LSNKHFQILXXXXXXLLNDISTNGTWL-NGQKVEK 52
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 397;
                                                                                         Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.3%; Score 65; DB 2; Length 579; 29.4%; Pred. No. 2.8; ive 11; Mismatches 23; Indels
                                                                                                                                                 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34; Indels
                                                                                      ; Score 66.5; DB 2;
; Pred. No. 0.66;
17; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
19.5%; Score 65.5; DE
Best Local Similarity 28.0%; Pred. No. 1.6;
Matches 21; Conservative 11; Mismatches
                                                                                      19.8%;
26.4%;
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Best Local Similarity 29.4%;
Matches 20; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 NSNQLLSQGDEITVG 67
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                                                                                                                     Best Local Similarity 26.4% Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                              99
                                                                                                                                                                                                                                                                                                                                                                   FERLSHGDRLSL 96
                                                                                                                                                                                                                                                                                                                              55 NQLLSQGDEITV
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A; Residues: 1-579 < WAD>
C;Genetics:
A;Gene: BH1777
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                                                                                      Query Match
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63 EITVG 67

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FGRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI--STNGT--WLNGQKVEKNSNQLL 58

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C;Accession: T00393
R;Matsuura, S.; Tauchi, H.; Nakamura, A.; Kondo, N.; Sakamoto, S.; Endo, S.; Smeets, D.;
Rature Genet. 19, 179-181, 1998
A;Title: Positional cloning of the gene for Nijmegen breakage syndrome.
A;Reference number: Z14144; MUID:9828099; PMID:9620777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 8q21
A;Introns: 13/1, 57/3; 107/2; 160/3; 195/2; 234/3; 299/2; 332/1; 375/2; 466/2; 615/3; 63
C;Superfamily: human Nijmegen breakage syndrome protein NBS1
C;Keywords: DNA repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable ABC transporter Rv1747 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: D70986
B;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Comnor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Atlile: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295997; PMID:9634230
A;Accession: D70986
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: Mycobacterium tuberculosis probable ABC transporter Rv1747; ATP-binding
                                                                                                                                                                                                                                Nijmegen breakage syndrome protein NBS1 - human
NiAlternate names: cell cycle regulatory protein p95
C.Species: Homo sapiens (man)
C.Species: 01-Peb-1999 #sequence_revision 01-Peb-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:060934; EMBL:AB013139; PIDN:BAA28616.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 62; DB 2; Le
Pred. No. 9.1;
7; Mismatches 13;
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hypothetical protein T211.110 - Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 LKDNSKYGTFVNEEKMONGFSRTLKSGDGITFG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 INDISTNGTWINGQKVEKNSNQLLSQGDEITVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Mismatches
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SINGTFVNGARVDA---ALLHDGDVVTIG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 STNGTWINGOKVEKNSNQLLSQGDEITVG 67
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ilarity 39.4%;
Conservative
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|||::: |
481 SNQVVALG 488
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Best Local Similarity
Matches 13; Conserv
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hes 13; Conserv
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                                                                                                                                                                                                                   FHA domain [imported] - Chlamydophila pneumoniae (strain J138)

C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: B86579
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: B86579
A;Accession: B86579
A;Residues: 1-845 <STO>
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A; Residues: 1-845 <a href="ARCAGE">ARCAGE ARCAGE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q927J3; GB:BA000008; NID:g8979084; PIDN:BAA98919.1; GSPDB:GN
A;Experimental source: strain J138
C;Genetics:
A;Gene: CPj0712
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A;Molecule type: DNA
A;Residues: 1-845 <REA>
A;Cross-references: GB:AE002167; GB:AE002161; NID:g7188971; PIDN:AAF37929.1; PID:g718897
A;Experimental source: strain AR39, HL cells
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18.8%; Score 63; DB 2; Length 845;
Best Local Similarity 29.4%; Pred. No. 7.6;
Matches 20; Conservative 19; Mismatches 21; Indels
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Best Local Similarity 29.4%; Pred. No. 7.6;
Matches 20; Conservative 19; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | | ::: |
SNQVVALG 488
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| :|
514 VIRLG 518
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A,Cross-references: UNIPROT:Q06001; EMBL:U19027; NID:g609363; PID:g609364; GSPDB:GN00012.
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NyAltenate names: hypothetical protein L8083.1
C.Species: Saccharomyces cerevisia protein L2083.2
C.Species: 23-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: MIPS:YLR238w
A;Cross-references: SGD:S0004228
A;Map position: 12R
C;Keywords: transmembrane protein
F;455-471/Domain: transmembrane #status predicted <TVM>
               A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 LSQGDEITVG 67
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Matches 11; Conserv
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A;Molecule type: DNA
A;Residues: 1-478 <HAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable membrane protein, containing PHA domain [imported] - Clostridium acetobutylicum (Species: Clostridium acetobutylicum (Species: Clostridium acetobutylicum (Species: Clostridium acetobutylicum (Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacession: D96904 (Spacess
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A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
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A;Introns: 411/2; 456/2; 504/3; 604/3; 685/1; 731/3; 768/3; 786/1; 822/3; 865/3; 895/3
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Datession: T49879
S;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Submitted to the Protein Sequence Database, April 2000
A;Reference number: 224493
A;Accession: T49879
A;Accession: T49879
A;Molecule type: DNA
A;Retus: preliminary
A;Molecule type: DNA
A;Residues: 1-1075 <-BEV>
A;Experimental source: UNIPROT: Q9LY20; EMBL: AL163912; GSPDB: GN00063; ATSP: T2II.110
A;Experimental source: cultivar Columbia; BAC clone T2II
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T19167
T19167
T19167
Cipecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispate: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 09-Jul-2004
CiAccession: T19167
RiAinscough, R.
Submitted to the BMBL Data Library, July 1995
A;Reference number: Z19082
A;Accession: T19167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----NDI----STNGTWLNGQKVEKNSNQLLSQGDEI 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 61.5; I
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 18.3%;
1 Similarity 23.5%;
24; Conservative 1.
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IRNGDTI 456
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Best Local Similarity
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A; Molecule type: DNA
A; Residues: 1-150 <WILD>
A; Residues: 1-150 <WILD>
A; Cross-references: UNIPROT: Q9U3Q2; EMBL: Z50109; PIDN: CAB54192.1; GSPDB: GN00020; CESP: CO:
A; Experimental source: clone C09H10
C; Genetics:
A; Gene: CESP: C09H10.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: UNIPROT:Q19846; EMBL:U49829; NID:g1203924; PID:g1203931; PIDN:AAA9338(
C; Genetics:
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A;Introns: 8/1; 52/3; 74/1; 96/1; 128/2; 149/3; 199/2; 255/3; 297/3; 319/3; 350/3; 390/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                              3 FGR-NPAC----DYHLGNISRLSNKHFQILXXXXXXLLNDISTNGTWLNGQKVEKNSNQL 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F27D9.8 - Caenorhabditis elegans Cipacies: Caenorhabditis elegans Cipacies: Caenorhabditis elegans C.Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004 C;Accession: Ti6191 R;Bentley, D. R;Bentley, D. Submitted to the EMBL Data Library, February 1996 A;Description: The sequence of C. elegans cosmid F27D9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                   A,Map position: 2
A,Introns: 15/1; 58/3
C,Superfamily: Caenorhabditis elegans hypothetical protein C09H10.10
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                                                                                                                                                                                                                                                                                                                     DB 2; Length 150;
                                                                                                                                                                                                                                                                                                                                                                                31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: T16191
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                  'Match 17.9%; Score 60; DB 2
Local Similarity 27.1%; Pred. No. 2.8;
tes 19; Conservative 12; Mismatches
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C;Species Caenorhabditis elegans
C;Species Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: D88188
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: D88188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       penicillin-binding protein 1B mrcB - Synechocystis sp. (strain PCC 6803)
N;Alternate names: protein slr110
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S75331
K;Aneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S75331
A;Attus: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-749 <KAN>
A;Residues: 1-749 <KAN>
A;Residues: 1-749 <KAN>
A;Residues: 1-740 <KAN>
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A;Note: similar to E. faecium initiation factor (IF-2)
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    17.9%; Score 60; DB 2; Length 478; 30.5%; Pred. No. 10; ive 15; Mismatches 20; Indels
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C, Superfamily: penicillin-binding protein
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A;Molecule type: DNA
A;Residues: 1-192 <STO>
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OM protein - protein search, using sw model

Run on:

February 24, 2005, 15:04:15; Search time 125.285 Seconds (without alignments) 273.851 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-936-956-19 336 1 WTFGRNPACDYHLGNISRLS.....QKVEKNSNQLLSQGDEITVG 67

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 segs, 512079187 residues Searched:

Total number of hits satisfying chosen parameters:

1612378

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	saccharomyc					-) arabidopsis) neurospora	_		Clostridium	2 schizosacch	1 pseudomonas	_		2 rhodopirell
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do	Query	93.3	93.3	81.4	9.69	69.5	50.9	40.9	40.9	34.5	34.2	33.3	31.4	31.1	29.9	29.2	29.3	28.3	27.8	27.8	27.5	27.1			26.5	26.0	25.9	25.7	25.4	25.3	25.3	25.0
	Score	313.5	313.5	273.5	234	233.5	171	137.5	137.5	116	115	112	105.5	104.5	100.5	66	98.5	95	93.5	93.5	92.5	91	O.	89.5	89	87.5	87	86.5	85.5	85	85	84
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Q81013 mus musculu Q6nhd4 corynebacte Q6nhg7 corynebacte Q8fuh9 corynebacte Q6mg14 bdellowibri Q8frj5 corynebacte Q8nu92 corynebacte Q6ns042 corynebacte Q8nu92 corynebacte P46012 caenorhabdi Q8u7w4 agrobacterii Q14270 echizosacch Q73zrl mycobacterii P64897 mycobacterii
CHFR MOUSE Q6NHD4 Q6NKG7 Q6NKG7 Q6FU49 Q6FU49 Q6FU45 Q8FU55 Q8NU92 XCM9V2 XK15_CAEEL Q8U7W4 YK78_SCHPO Y127_MYCTU X127_MYCTU X158_MYCRO
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## ALIGNMENTS

YEAST STANDARD; 6; G-1991 (Rel. 19, Creat	(Rel. (Rel. onine-p	Ariuse 17.) Name=RAD53; Synonyms=MEC2, SAD1, SPK1; OrderedLocusNames=YPL153C; NBTNames=D7568.	Saccharomyces cevisiae (Baker's yeast).	<pre>Bukaryota; Fung1; ABComyCota; SaccharomyCot1na; SaccharomyCeres; SaccharomyCetales; SaccharomyCetaceae; SaccharomyCes.</pre>	NCB1_TaxiD≂4932; [1]	SEQUENCE FROM N.A. MEDLINE-91117267: PubMed=1899289;	Stern D.F., Zheng P., Beidler D.R., Zerillo C.,	"Spki, a new kinase from saccharomyces cerevisiae, phospholytates proteins on serine, threonine, and tyrosine.";	Cell. Biol. 11:987-1001(1991).	[2] Sections from N a	IN=S288c / AB972;	MEDLINE=97103777;		"The sequence of 55 kb on the left arm of yeast chromosome XVI identifies a small muclear RNA, a new putative protein kinase and two		Yeast 12:1483-1492(1996).	[3] SEOUENCE FROM N.A.	STRAIN=5288C / AB972;	13271; PubMed=9169875; Storms D V Abmed A Albermann V Allen R Ansorge W	jo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,	tein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,	g E., Churcher C.M., Coscer F., Davis K., Davis K.M., rich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,	an M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,	J., Hebling U., Heumann K., Hilbert H., Hillier L.W.,	A Hunicke-Smith S., Hyman K., Johnston M., Maiman S., Mieine M., A Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,	the R., Messenguy F., Mewes HW., Mirtipati S., Moestl D.,	ler-Auer S., Namath A., Nentwich U., Oefner P., Pearson D.,	rene B. Ochramm C. Ochrader M., Schaler M., Schale M.,	starazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,	h S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E.,	g W.W., Zollner A., Vo D.H., Hani J.;	"The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI."; Mature 187:101-106 (1997)
T 1 YEAS: P222: 01-A	01-AUG-1991 25-OCT-2004 Serine/thre	Name=RADS	Saccharom	Saccharom	NCB1_Tax1 [1]	SEQUENCE MEDLINE=9	Stern D.F	"Spki, a proteins	Mol. Cell	[2] SEOTENCE	STRAIN=S288C	MEDLINE=9	Purnelle	"The segu	new putat	Yeast 12:	[3] SEOUENCE	STRAIN=S2	MEDLINE=9	Araujo R.,	Botstein	Chung E., Dietrich	Duncan M.	Hall J.,	Komp C.,	Marathe R	Mueller-A	Scherene	Urrestara	Walsh S.V	Zhong W.W	The nuct
RESULT RA53 YI ID RA AC PR	5000	8 8 8	ខ្លួ	888	Z Z	R. X.	RA :	RT	RE	N C	RC.	X X	2 2	E E	Z.	Z.	R R P G	22	X 6	<b>5 2</b>	R.	<b>\$</b> \$	RA	8	\$ £	RA	2 2	<b>§</b> 6	<b>5 2</b>	RA R	RA I	RT

FUNCTION

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GermOnline, 144135, ...
GermOnline, 144135, ...
SGD: S000006074; RAD53.
GO; GO:0006534; C:nucleus; IDA.
GO; GO:0004712; F:protein threonine/tyrosine kinase activity; IDA.
GO; GO:0006281; P:DNA repair; IMP.
GO; GO:0006139; P:nucleobase, nucleoside, nucleotide and nucl. ..; IGI.
                                                                                                                                                                                                                                    Pfam; PF0048; PHA; 2.
Pfam; PF00069; PHA; 2.
Pfam; PF00069; Pkinae; 1.
Prodom; PF000061; Prot. kinase; 1.
SWART; SW00240; FHA; 2.
SWART; SW00220; STKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00101; PROTEIN CINASE DOM; 1.
PROSITE; PS00101; PROTEIN CINASE ST; 1.
PROSITE; PS00108; PROTEIN CINASE ST; 1.
PROSITE; PS00108; PROTEIN CINASE ST; 1.
Phosphorylation; Repeat; Serine/threonine-protein kinase; Transferase;
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Protein kinase.
FHA 2.
ATP (By similarity).
ATP (By similarity).
Proton acceptor.
                                                                                                                                       InterPro; IPR000253; FHA.
InterPro; IPR011009; Kinase like.
InterPro; IPR000719; Proc Kinase.
InterPro; IPR008271; Ser Lhr Dkin AS.
InterPro; IPR002290; Ser Lhr Dkinase.
InterPro; IPR008984; SMAD FHA.
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                .K3Q; NMR; A=14-164.
.QU5; NMR; A=549-730.
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PDB; 1K3N; N
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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X Kim E.M., Jang Y.K., Park S.D.;

A Kim E.M., Jang Y.K., Park S.D.;

A Kim E.M., Jang Y.K., Park S.D.;

A Kim E.M., Jang Y.K., Park S.D.;

A Kim E.M., Jang Y.K., Park S.D.;

Saccharomyces cerevisiae, is dependent upon Rad53 kinase.";

I Saccharomyces cerevisiae, is dependent upon Rad53 kinase.";

I Saccharomyces cerevisiae, is dependent upon Rad53 kinase.";

I Nucleic Acids Res. 30:643-648 (2002).

I Nucleic Acids Res. 30:643-648 (2002).

I Nucleic Acids Res. 30:643-648 (2002).

C -1- FUNCTION: Controls S-phase checkpoint as well as G1 and G2 DNA damage checkpoints. Prevents entry into anaphase and mitotic exit after DNA damage via regulation of the Polo kinase CD5. Seems to be involved in the phosphorylation of RPH1.

C -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

C -1- CATALYTIC ACTIVITY: And P a protein = ADP + a phosphoprotein.

C -1- FTM: Autophosphorylated.

C -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

C -1- SIMILARITY: Contains 2 FHA domains.
                                                                                                                                                                                                                                                     PHÖSPHORYLATION.
MEDIATNE=2013167; PubMed=10562568; DOI=10.1033/emboj/18.22.6561;
MEDIATNE=20131667; PubMed=10562568; Marini F., Lopes M., Plevani P., Romano A., Di Fiore P.P., Foiani M.;
Romano A., Di Fiore P.P., Foiani M.;
"Activation of Rad53 kinase in response to DNA damage and its effect in modulating phosphorylation of the lagging strand DNA polymerase.";
EMBO J. 18:6561-6572(1999).
                                                                                                                                       MEDLINE=20018334; PubMed=10550056; DOI=10.1126/science.286.5442.1166; Sanchez Y., Bachant J., Wang H., Hu F., Liu D., Tetzlaff M., Elledge S.J.;
Elledge S.J.;
"Control of the DNA damage checkpoint by chkl and rad53 protein kinases through distinct mechanisms.";
                                      Allen J.B., Zhou Z., Siede W., Friedberg B.C., Elledge S.J.;
"The SAD1/RAD53 protein Kinase controls multiple checkpoints and DNA damage-induced transcription in yeast.";
Genes Dev. 8:2401-2415(1994).
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20057864; PubMed=10588905; DOI=10.1006/jmbi.1999.3313; Liao H., Byeon I.-J.L., Tsai M.-D.; Struction of a new phosphopeptide-binding domain containing the FHAZ of Rad53."; J. Mol. Biol. 294:1041-1049(1999).
                               WEDLINE=95047382; PubMed=7958905;
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1 IFHQ; NWR; A=573-730.

1 IFHR; NWR; A=1-164.

1 IGGG; X-ray; A/B=29-155.

1 JJ4K; NWR; A=573-730.
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EMBL; X96770; CAA65568.1; -.
EMBL; Z73509; CAA97858.1; -.
PIR; A39616; A33616.
PDB; 1DMZ; NMR; A=573-730.
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PRELIMINARY;
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QGDEITVG 133
60 QCDEITVG 67
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                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=284593;
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Local Si.
53;
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                                                                                                                                                                              66 WIFGRNPACDYHLGNISRLSNKHFQILLGEDGNLLLINDISTNGTWLNGQKVEKNSNQLLS 125
                                                                                                                                                     1 WTFGRNPACDYHLGNISRLSNKHFQI-LXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLS 59
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                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Marsischky G., Rolfs A., Richardson A., Kane M., Baqui M., Taycher F.
Hu Y., Vannberg F., Weger J., Kramer J., Moreira D., Kelley F.,
Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Kinase; Serine/threonine-protein kinase; Transferase. 821 AA; 91934 MW; AAB353DC7DF68119 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LaBaer J.;

"Creation of the YELEX clone resource: cloning of Saccharomyces cerevisiae ORFs in the Gateway recombinational cloning system.";

Submitted (JUL-2004) to the BMBL/GenBank/DDBJ databases.

-! SIMILARITY: Belongs to the Ser/Thr protein kinase family.

EMBL; AV693009; AAT93028.1;

SGD; S000006074; RADS3.

GO; GO:0004674; RADS3.

GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.

GO; GO:0004674; F:protein exine/threonine kinase activity; IEA.

GO; GO:0004648; P:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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                                                              93.3%; Score 313.5; DB 1; Length 821;
89.7%; Pred. No. 7e-32;
iive 0; Mismatches 6; Indels 1;
                                                                           76-32;
76-32;
~heg 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                  821 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00240; FHA; 2.
SMART; SM00220; S_TKC; 1.
SMART; SM0019; TyrKC; 1.
PROSITE; PS50006; FHA DOMAIN; 2.
PROSITE; PS0011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000253; FHA.
InterPro; IPR000253; FHA.
InterPro; IPR000719; Winase like.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008719; Prot kinase.
InterPro; IPR008719; Ser Lhr pkinase.
InterPro; IPR008174; Ser Lhr pkinase.
InterPro; IPR008145; Tyr pkinase.
Fam; PP00498; FHA; 2.
Pfam; PP00498; PHA; 2.
ProDom; PP000001; Prot_kinase; 1.
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                                                                                                            61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                    QGDEITVG 133
                                                                                                                                                                                                                                          QGDEITVG 67
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                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4932;
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25-OCT-2004
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Best Local 8
                                                              Query Match
                                                                                       Local
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ORFNames=KLLA0F11143g;
Kluyveromyces lactis NRRL Y-1140.
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                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=NRRL Y-1140;
                                                                                    SEQUENCE FROM N.A.
STRAIN=NRRL Y-1140;
                                                            NCBI_TaxID=284590;
                                                                                                                   Genolevures;
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Q6BUB2;
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QGBUB2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            $5-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Kluyveromyces lactis strain NRRL Y-1140 chromosome F of strain NRRL Y-
1140 of Kluyveromyces lactis.
                                                                                                                                                                                                                                                                                                                                                                                                                                       R GO; GO; UOUGABER; F; PICOCEIN AMINO ACIG PROSPROTYLATION; 1EA.

R INTERPRO; IPRO1009; Kinase like.

R INTERPRO; IPRO1009; Kinase like.

R INTERPRO; IPRO1019; FPAC, Kinase.

R INTERPRO; IPRO1229; Ser_thr_pkinase.

R INTERPRO; IPRO1245; Tyr_pkinase.

R INTERPRO; IPRO1245; Tyr_pkinase.

R INTERPRO; IPRO1245; Tyr_pkinase.

R INTERPRO; IPRO1245; Tyr_pkinase.

R PFAM; PRO0069; PKINASE; 1.

R PROMOF, PRO00001; PTAC kinase; 1.

R MART; SM00240; FHA; 2.

R SMART; SM00240; FHA; 2.

R SMART; SM0019; TYRC; 1.

R SMART; SM0019; TYRC; 1.

R PROSITE; PS50010; PROTEIN KINASE ATP; 1.

R PROSITE; PS50101; PROTEIN KINASE ST; 1.

R R PROSITE; PS50101; PROTEIN KINASE ST; 1.

R R PROSITE; PS50101; PROTEIN KINASE ST; 1.

R R PROSITE; PS50101; PROTEIN KINASE ST; 1.

R R PROSITE; PS50101; PROTEIN KINASE ST; 1.

R R PROSITE; PS50101; PROTEIN KINASE ST; 1.

R R PROSITE; PS50101; PROTEIN KINASE ST; 1.

R R PROSITE; PS50101; PROTEIN KINASE ST; 1.

R R PROSITE; PS50101; PROTEIN KINASE ST; 1.

R R PROSITE; PS50101; PROTEIN KINASE ST; 1.

R R PROSITE; PS50101; PROTEIN KINASE ST; 1.

R R PROSITE; PS50101; PROTEIN KINASE ST; 1.

R R PROSITE; PS50101; PROTEIN KINASE ST; 1.
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                                                                                                                                                                                    Ashbya gossypii (Yeast) (Eremothecium gossypii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Eremothecium.
                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                     STRAIN=ATCC 10895;
Brachat S., Voegeli S.E., Dietrich F.S., Lerch A., Gaffney T. Philippsen P.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AE016816; AAS51368.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.6%; Score 234; DB 2; Length 837;
66.7%; Pred. No. 1.7e-21;
tive 6; Mismatches 15; Indels
                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                     837 AA.
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                                                                                     PRT;
                                                                                                              05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
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                                                                                    PRELIMINARY;
                                                                                                 Q75CE9;
05-JUL-2004 (TrEMBLrel.
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|||||||||||||||
QGDEITVG 132
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Best Local Similarity
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                        ORFNames=ACR142W;
                                                                                                                                                                                                                               NCBI_TaxID=33169;
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AGD; ACR142W
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66 WIFGRNQGCDYYLGDISRLSNRHFMLMLGEEGTLMLKDTSTNGTWLNGARIQKDTNHILT 125
                                                                                                                                                                                                                                                     Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A dofontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
A doffaatd N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Blaykasten C.,
A Despons L., Fabre E., Fairhead C., Cenfanioleri F., de Daruvar A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Micaud J.M., Nikolski M., Oztas S., Ozter-Kalogeropoulos O.,
A Nicaud J.M., Nikolski M., Oztas S., Ozter-Kalogeropoulos O.,
A Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Witth B.,
Seniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
A Wincker P., Souciet J.L.,
T. "Genome evolution in yeasts.",
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SMART; SM00240; FHA; 2.
SMART; SM00210; STKC; 1.
SMART; SM00210; STKC; 1.
SMOSTIS; SS00019; TYKC; 1.
PROSITE; PS500107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
ATP-binding; Kinase; Serine, threonine-protein kinase; Transferase.
SEQUENCE 813 AA; 91482 MW; 949935699288789E CRC64;
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Kluyveromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; CR382126; CAG98295.1; -.
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69.5%; Score 233.5; DB 2; Length
Best Local Similarity 60.3%; Pred. No. 1.9e-21;
Matches 41; Conservative 13; Mismatches 13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000253; FHA.
InterPro; IPR011009; Kinase like.
InterPro; IPR011009; Kinase like.
InterPro; IPR000139; Prot kinase.
InterPro; IPR008271; Ser thr pkinase.
InterPro; IPR008984; SMAD FHA.
InterPro; IPR008984; SMAD FHA.
InterPro; IPR001245; Tyr pkinase.
Pfam; PP00498; FHA, 2.
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phase."
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                                                                                                                                                                             Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
A Barnay S., Blanchin S., Beckerich JWM., Beyne B., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lebur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellonz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Wincker P., Souciet J.L.,
T., "Genome evolution in yeasts.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 WIFGRNPACDYHLGNISRLSNKHFQILXXXXXXLL--NDISTNGTWLNGQKVEKNSNQLL 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prodom; Provos; Farinase; 1.

SMART; SM00240; FHA; 2.

SMART; SM00220; TKC; 1.

SMART; SM00219; TYRK; 1.

PROSITE; PS50019; PROTEIN KINASE ATP; 1.

PROSITE; PS50011; PROTEIN KINASE ATP; 1.

PROSITE; PS00109; PROTEIN KINASE ATP; 1.

PROSITE; PS00109; PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
                                                                                 Eukaryotta, Saccharomycottas, Saccharomycotina, Saccharomycetes, Saccharomycetales, Saccharomycetaceae, Debaryomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000467+; F:protein: serine/threonine kinase activity; IEA
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.9%; Score 171; DB 2; Length 751; 50.7%; Pred. No. 2.6e-13; ive 9; Mismatches 23; Indels
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last anotation update)
Similar to sp|P22216 Saccharomyces cerevisiae YPLI53c SPK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 751 AA; 85411 MW; EF8A15F56A788346 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000253; FHA.
InterPro; IPR011009; Kinase like.
InterPro; IPR011009; Kinase like.
InterPro; IPR000719; Prot Kinase.
InterPro; IPR0002290; Ser thr pkinase.
InterPro; IPR008984; SMAD FHA.
InterPro; IPR008984; SMAD FHA.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00498; FHA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CR382135; CAG86283.1; -.
                                                  (Fragment).
ORFNames=DEHAOC13211g;
Debaryomyces hansenii CBS767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 50.7 tes 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  Nature 430:35-44(2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQGDEITVG 67
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                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                         STRAIN=CBS767;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
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60 WRPGRHKSCEVVL-NGPRVSNFHPEIYQGHRNDSDESENVVFLHDHSSNGTFLNFERLAK 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                "Evolutionary conservation of a splice variant of the Cds1/Chk2 kinase restricted to its regulatory domain.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ783838; CAH04269.1;
GO; GO:0016301; F:kinase activity; IEA.
InterPro; IPR0100253; FHA.
InterPro; IPR01009; Kinase like.
InterPro; IPR000199; Fort Kinase.
InterPro; IPR000994; SMAD_FHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Serine/threonine-protein kinase cds1 (EC 2.7.1.37) (Checkpoint kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A kinase from fission yeast responsible for blocking mitosis in S
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., FUNCTION, INTERACTION WITH RAD26, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND FUNCTION.
MEDLINE=95240713; PubMed=7723827; DOI=10.1038/374817a0;
Murakami H., Okayama H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 204 AA; 23162 MW; 85FC79F7553B632D CRC64;
                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                    Last annotation update)
                                                                                        Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  460 AA.
   204 AA
                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD000001; Prot_kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50006; FHA_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 NSRTILSNGDEIRIG 133
                                                     25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 NSNOLLSQGDEITVG 67
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 374:817-819(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00498; FHA; 1.
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                                                                                                                                                                                                                                                                                                     Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Ducommun B.;
                                                                                                                                                 Cds1 kinase
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PD000001; Prot_kinase; 1.
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CONFLICT
CONFLICT
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BINDING
                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                        Query Match
 ProDom;
                                                                                                                                                                              DOMAIN
                                                                                                                                                               DOMAIN
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                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                             Lindsay H.D., Griffiths D.J.F., Edwards R.J., Christensen P.U., Murray J.M., Osman F., Walworth N., Carr A.M.; "S-phase-specific activation of Cds1 kinase defines a subpathway of the checkpoint response in Schizosaccharomyces pombe."; Genes Dev. 12:382-395(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: Autophosphorylated.
SIMILARITY: Belongs to the Ser/Thr protein kinase family. CDS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 while DNA synthesis is in progress.
CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
SUBUNIT: Interacts with rad26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP, 000534; 1JOW.
GeneDB_SPombe; SPCC18B5.11c; -.
InterPro; IPR000523; Finase.
InterPro; IPR0101009; Kinase like.
InterPro; IPR001019; Prot kinase.
InterPro; IPR002101; Ser_thr_pkin_AS.
InterPro; IPR002230; Ser_thr_pkinase.
InterPro; IPR002230; Ser_thr_pkinase.
InterPro; IPR012345; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Contains 1 FHA domain.
                MEDLINE=98119835; PubMed=9450932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ222869; CAA11019.1; -. EMBL; AL109736; CAB52158.1; -. PIR; S58882; S58882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X85040; CAA59410.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00498; FHA; 1.
Pfam; PF00069; Pkinase; 1.
                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subfamily
                                                                                                                                                               STRAIN=972
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1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 WTFGRNPACDYHLGNISRLSNKHFQIL-----XXXXXXLLNDISTNGTWLNGQKVEK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 WIFGRNPACDYHLGN-----ISRLSNKHFQILXXXXXXLLNDISTNGTWLNGQKVEK 52
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pfam; PF0069; Pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
SWART; SM00240; FHA; 1.
SWART; SM00210; FTA; 1.
PROSITE; PS50006; FHA DOMAIN; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 503 AA; 56699 MW; BC01BF3D8E4CEC71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
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60
                                                                                                                                                                                                   Protein kinase.
ATP (By similarity).
ATP (By similarity).
Proton acceptor (By similarity).
R -> G (in Ref. 1).
F -> C (in Ref. 1).
W, 4CEB963D3376DB54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 460;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                               Query Match
40.9%; Score 137.5; DB 1;
Best Local Similarity 41.3%; Pred. No. 3.6e-09;
Matches 31; Conservative 13; Mismatches 22;
SMART; SM00240; FHA; 1.
SMART; SM00220; S TKC; 1.
PROSITE; PS50006; FHA_DOMAIN, 1.
PROSITE; PS500107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS50011; PROTEIN KINASE ST; 1.
APP-binding; Cell cycle; Phosphorylation; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        503 AA.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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                                                                                                                                                                                     FHA.
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433
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                                                                                                                                                                                                                                                                                                                   238 ;
460 AA;
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NCBI_TaxID=7955;
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91 YSFGRDKRCDYSFSNSILKKSPYFNTYSKKHPRIFRDENLYYLEDLSGNGTWYDDEKLGN 150
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
A Goffard N., Frangeul L., Aigle M., Anthourd V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bleykaaten C.,
B Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Roszul R., Lafarhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Janniaux N., Joyer P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Ortas S., Ozier-Kalogeropoulos O.,
Pellonz S., Potier S., Richard E., Straub M.L., Suleau A.,
Swennene D., Tekaia P., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
I "Genome evolution in yeasts.";
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Lu Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

-1-SIMILARITY: Belongs to the Ser/Thr protein kinase family.

EMBL; CR382132; CAG78745.1;

EMBL; CR382132; CAG78745.1;

EMBL; CR00004674; F: Protein-tyrosine kinase activity; IEA.

GO; GO:000046713; F: Protein-tyrosine kinase activity; IEA.

GO; GO:000046713; F: Protein-tyrosine kinase activity; IEA.

GO; GO:0000468; P: Protein amino acid phosphorylation; IEA.

InterPro; IPR001009; Kinase like.

InterPro; IPR001299; EMA.

InterPro; IPR001299; Ser_Thr_pkinase.

InterPro; IPR001249; FHA.

InterPro; IPR001249; FYA.

InterPro; IPR00149; FYA.

InterPro; IPR00149; FYA.

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INTERPRO; IPR00149; FYA.

INTERPRO; IPR00149; FY
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Similar to DEHAOC13211g Debaryomyces hanseni. Shimilar to DEHAOC13211g Debaryomyces hansenii. Yarrowia lipolytica CLIB99.
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                                                                                                                                                                                                                                                                                                                                                                                     898 AA
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                                                                                                                                                                                          151 GKOSLLSNNSVIAL 164
                                                                                                                   53 NSNOLLSQGDEITV 66
                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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06 C079

10 C079

10 D7 C25-0C

D7 25-0C

D7 25-0C

D7 25-0C

D8 Simil

D8 Simil

C8 Simil

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STAIN=AB, TISSUB=Whole body;

MEDLINE=2238257; PubMed=1247932; DOI=10.1073/pnas.242603899;

A Straubberg R.D., Feingold B.A., Grouse L.H., Derge J.G.,

A Straubberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.P., Zebebrg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heishe F.,

B pitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

B rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R aha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Rosak S.A., McEwan P.J., McKernan R.J., Malke J.A., Gunaarane P.H.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Myting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"T "Generation and initial analysis of more than 15,000 full-length human and man and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and manger and man
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                                                                                                                                                                        82 WTFGRAGSANFVVARKARLSKIHFIVEHTGGTKQRAGTVVIRDVSLNGTSVNGRYLGRGN 141
                                                                                                                        1 WTFGRNPACDYHLGNISRLSNKHFQI-----LXXXXXXLLNDISTNGTWLNGQKVEKNS 54
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Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                               6; Gaps
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GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR00259; FHA.
InterPro; IPR00109; Kinase like.
InterPro; IPR00109; For kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkinase.
InterPro; IPR008894; SMAD_FHA.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Pfam; PF00069; PKinase; 1.
ProDom; PD00001; Prot_kinase; 1.
SMART; SM00240; FHA; 1.
                                                                                                                                                                                                                                                                                                                                       SALLQNGDVITVG 154
                                                                                                                                                                                                                                                                                        55 NOLLSOGDEITVG 67
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Q803E2
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2 TFGRNPACDYHLGNISR-LSNKHFQILXXXXXXLLNDISTNGTWLNG--QKVEKNSNQLL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 TFGRSEQCDWTLPDPERVISGTHGELIKFGDKYLIKDLSTNGTFVNNAVTPIGQGNELAL 92
                                                                                                                                                                                                             MEDILINE=22508454; PubMed=12260739; DOI=10.1016/S0140-6736(03)12659-1; Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K., Iijima Y., Najima M., Nakano M., Yamashitra A., Kubota Y., Kimura S., Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.; "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae."; Lancet 361:743-749(2003).
                                                                          Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                                                                                                            EMBL, AP05087; BAC62386.1; -.
InterPro; IPR000253; FHA.
InterPro; IPR0884; SNAD_FHA.
SMART; SM00240; FHA; 1.
SMART; SM00240; FHA; 1.
SCOMPLETE, PSS0006; FHA; 1.
SCOMPLETE PSS0006; FHA; 1.
SEQUENCE 398 AA; 44741 MW; 419A55457EB4D173 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.1%; Score 104.5; DB 2;
33.3%; Pred. No. 6.2e-05;
tive 16; Mismatches 27;
                                                                                                                                                                                            STRAIN=RIMD 2210633 / Serotype 03:K6;
         Hypothetical protein VPA1043
                                 OrderedLocusNames=VPA1043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23; Conservative
                                                     Vibrio parahaemolyticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | || : :|
93 SHGDTVALG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 SQGDEITVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mesorhizobium loti.";
                                                                                                  Vibrionaceae: Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      359 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome. SEQUENCE 359 AA;
                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mlr2358 protein.
                                                                                                                        NCBI_TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q98IK6;
01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                       1 WTFGRNPACDYHLGN-----ISRLSNKHFQILXXXXXXLLNDISTNGTWLNGQKVEK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 GRNPACDYHLGNISR-LSNKHFQILXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLSQGD 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-RIMD 2210633 / Serotype O3:K6;
STRAIN-RIMD 2210633 / Serotype O3:K6;
MEDLINE-22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
MEDLINE-22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
Makino K., Oshima M., Kurokawa K., Yokoyama K., Kubota Y., Kimura K.,
Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
Lancet 361:743-749(2003).
                                                                                                                                                                                                                    Gaps
SMART; SM00220; S_TKC; 1.
PROSITE; PS50006; FHA DOMAIN; 1.
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN KINASE_ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 503 AA; 56657 MW; 351A24EA5BBAFBD5 CRC64;
                                                                                                                                                                                                                    œ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.4%; Score 105.5; DB 2; Length 504; 35.4%; Pred. No. 5.9e-05; ive 14; Mismatches 27; Indels 1;
                                                                                                                                                                    33.3%; Score 112; DB 2; Length 503; 31.1%; Pred. No. 8.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio.
                                                                                                                                                                                                                 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome; Hypothetical protein.
SEQUENCE 504 AA; 55469 MW; 2F96C75A4F83648E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 24, Last sequence update) (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          504 AA
                                                                                                                                                                                                                 11; Mismatches
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PROSITE; PS50006; FHA_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP005078; BAC59674.1; -. HSSP; Q9GEP1, 1LGQ.
InterPro; IPR000253; FHA.
InterPro; IPR008994; SMAD_FHA.
Pfam; PF00499; FHA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein VP1411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 24, (TrEMBLrel. 24, (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                       151 GKQSLLGNNSVÍAL 164
                                                                                                                                                                                                                                                                                                                                                         53 NSNQLLSQGDEITV 66
                                                                                                                                                                                         Local Similarity 31.1 les 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OrderedLocusNames=VP1411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vibrio parahaemolyticus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 EITVG 67
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VVSLG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       087HC2;
01-JUN-2003
01-JUN-2003
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2003
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Q87HC2
ID Q87HC
AC Q87HC
DT 01-JU
DT 01-JU
                                                                                                                                                                                                                    Matches
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3;

27; Indels

Length 398;

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Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishikawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Maszaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 359;
                                                                                                                                                                                                             Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39374 MW; 36732CCBB6AB7DD5 CRC64;
                                                                                      Last sequence update)
Last annotation update)
359 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.9%; Score 100.5;
                                                             Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                              Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR000253; FHA.
Interpro; IPR00984; SMAD_FHA.
Pfam; PF00498; FHA; 1.
SMART; SM00240; FHA; 1.
PROSITE; PS50006; FHA_10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AP002999; BAB49510.1; -.
                                                      01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                    OrderedLocusNames=mlr2358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Res. 7:331-338(2000).
PRELIMINARY;
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Indele

36;

4; Mismatches

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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         Blr3598 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=USDA110;
                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003
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26;
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Q8DJ88
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Nausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
A ploking R.F., Jordan H., Moore T., Max J., Hang J., Haibe F.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Brownstein M.J., Usdin T.B., Tonahlyuki S., Carninci P., Frange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Brownstein M.J., Widnar P.B., Tochhyuki S., Carninci P., Frange C.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schnutz J., Myers R.M., Butterfield Y.S.,
A Nones S.J., Marra M.A.,
Jones S.J., Marra M.A.,
T "Generation and initial analysis of more than 15,000 full-length human
                                                                    9 CDYHLGNISR-LSNKHFQILXXXXXXLLNDISTNGTWLNGQKVEKNSNQLLSQGDEITVG 67
                                                                                             35 CDWTLSDPDKFISGRHCEIRYQAGTFWLHDVSRNGTFVNGSSQRMNAPHRLTQGDRLLIG 94
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                           Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 99; DB 2; Length 626; Pred. No. 0.00053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO:0000151; C:ubiquitin ligase complex, IEA.
GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO:0008270; F:zinc ion binding; IEA.
GO:0016567; P:protein ubiquitination; IEA.
                      25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klein S., Gerhard D.S.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
--- SINTLARITY: Contains 1 RING-type zinc finger.
EMBL BEOGG4721; AAH64721.1; ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Hypothetical protein MGC75959.
; Pred. No. 0.00018; 14; Mismatches 25
                                                                                                                                                                                                                                      626 AA
                                                                                                                                                                                                                                                                             -JUL-2004 (TrEMBLrel. 27, Created)
                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; IPR008984; SMAD_FHA.; IPR001841; Znf_ring.
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38.2%;
ilarity 33.3%;
Conservative 1
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                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kenopodinae; Xenopus.
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Best Local Similarity
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8364;
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                                                                                                                                                                                                                                                                                                                                                                             Name=MGC75959;
                 20;
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                         1 WTFGRNPACDYHLGNISRLSNKHFQIL -- XXXXXXLLNDISTNGTWLNGOKVEKNSNQLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.3%; Score 98.5; DB 2; Length 460; 35.4%; Pred. No. 0.00044; Live 12; Mismatches 29; Indels 1
                                                                                                                                                                                                                                                                                                                                        OrderedlocusNames-blr3598;
Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synechococcus elongatus (Thermosynechococcus elongatus)
Bacteria, Cyanobacteria, Chroococcales, Synechococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 460 AA; 50895 MW; C2CC7E01310D367F CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                         460 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                              Created)
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MEDLINE=22225144; PubMed=12240834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22484998; PubMed=12597275;
                                                                                                                                                                                                                                                                                                                                                                                                       Bradyrhizobiaceae; Bradyrhizobium
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InterPro, IPR008984; SMAD_FHA.
                                                                                                                                                                                                                                                              (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
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nes 23; Conservative
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                                                                                                                                                                                                                      PRELIMINARY;
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SMART; SM00240; FHA; 1.
                                                                                                                   94 KNGDVIYV 101
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RLTIG 97
                                                                             59 SQGDEITV
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Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AC068900; AAG12599.1; -.
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                                                                                                                            HSSP; P46014; 1MZK.
            Town C.D., Kaul S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F16B3.3 protein.
Name=F16B3.3;
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            Sasamoto S.,
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Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu
Maiti R., Konning C.M., Koo H., Fujii C.Y., Utterback T.R.,
Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                          Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1."; DNA Res 9:123-130(2002).

-I SIMILARITY: Belongs to the ABC transporter family. EMBL; AP005373; BAC08892:1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMAKK; SUNCATO, FIRS, J.
PROSITE; PS00211, ABC TRANSPORTER_1; UNKNOWN_1.
PROSITE; PS002013; ABC TRANSPORTER_2; 1.
PROSITE; PS50006; FHA_DOMAIN; 2.
ATP-binding; Complete_proteome.
SEQUENCE 1029 AA; 114450 MW; E4E6278B017BD179 CRC64;
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Town C.D., Kaul S.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
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01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein F11A12.9 (Fragment).
Name=F11A12.9;
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          567 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probom; PD000006; ABC_transporter; 1.
SMART; SM00382; AAA; 1.
SMART; SM00240; FHA; 3.
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01-MAR-2001 (TrEMBLrel. 16, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Best Local Similarity (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317 VGDSIRIG 324
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Town C.D., Kaul S.;
Submitted (OCT-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 QGDEITVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [4]
SEQUENCE FROM N.A.
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MR GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0003677; F:DNA binding; IEA.

R GO; GO:0003677; F:DNA binding; IEA.

R GO; GO:000555; P:CHEQUIATION of transcription, DNA-dependent; IEA.

R InterPro; IPR000894; FHA.

R InterPro; IPR008984; SMAD_FHA.

R Fam; PF00498; FHĀ; 1.

R SMART; SM00246; FHĀ; 1.

R RART; SM00246; FHĀ; 1.

R RASTTE; PS50006; FHĀ; 1.

R ROSTTE; PS50006; FHĀ; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 27.8%; Score 93.5; DB 2; Length 567; Best Local Similarity 29.9%; Pred. No. 0.0025; Matches 23; Conservative 15; Mismatches 28; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B., Wu
Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B., Wu
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.B.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AC021640; AAF32447.1;
HSSP; P46014; IMZK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GOS 0.0005634, Cincleus; IEA.
GOS, GO:0005634, Cincleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355, P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000637; A+T_hook.
InterPro; IPR000535; FHA.
InterPro; IPR008984; SMAD_FHA.
Pfam; PF02178; AT hook; 2.
Pfam; PF0498; FHA; 1.
SMART; SM00384; AT hook; 2.
SMART; SM00384; AT hook; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50006; FHA DOMAIN; 1.
SEQUENCE 585 AA; 66387 MW; DBDE57ADAD4ABD42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  585 AA
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Indels
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Last annotation update)
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Last annotation update)
21;
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Local Similarity 35.1%; Pred. No. 0.0034;
Nes 26; Conservative 13; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       434 AA.
  18; Mismatches
                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
Uncharacterized conserved protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2004 (TrEMBLrel. 26, Created) 01-MAR-2004 (TrEMBLrel. 26, Last seq 01-MAR-2004 (TrEMBLrel. 26, Last am Uncharacterized conserved protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OrderedLocusNames=VVA0995; Vibrio vulnificus (strain YJ016).
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                                                                                                                                                                                                                                                                                                                                                                                             OrderedLocusNames=VV20445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
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21; Conservative
                                                                                                                                                                                                                                                                    PRELIMINARY;
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SMART; SM00240; FHA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                  Vibrio vulnificus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                             SCDKL 76
                                                                                                                        60 QGDEI 64
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  Matches
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
B Barnay S., Blanchin S., Beckerich JM., Beyne E., Bleykaten C.,
B Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Royer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Hantraye E., Fahre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
A Hantraye F., Hemmequin C., Janniaux N., Joyer P., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Pukuhara M., Thierry A.,
A Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
T "Genome evolution in yeasts.",
19 SLGFKPGSTIRIGRIVRGNEIAIKDAGISTKHLRIVSDSENWIIHDLGSSNGTILNSDTI 78
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SMART; SW00220; STKC; 1.
SMART; SW00219; TYKC; 1.
SMART; SW00219; TYKC; 1.
PROSITE; PS50001; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 443 AA; 50501 MW; 80B5BACD8BAB9B9D CRC64;
                                                                                                                                                                                                                                                                                                                            Debaryomyces hansenii CBS767.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SIMILARITY: Belongs to the Ser/Thr protein kinase family. EMBL; CR382139; CAG90972.1; -
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.5%; Score 92.5; DB 2; Length 443; 32.3%; Pred. No. 0.0026;
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                     25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to CA4770|IPF9382.3 Candida albicans IPF9382.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000253; FHA.
InterPro; IPR011009; Kinase like.
InterPro; IPR000719; Prot Kinase.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR008271; Ser thr pkinase.
InterPro; IPR008984; SMAD FHA.
InterPro; IPR001245; Tyr pkinase.
Pfam; PP00498; FHA; 1.
Pfam; PP0069; Pkinase; 1.
                                                                                                                                                                                    PRT;
                                        67
                                                                SDIPVNLSHGDEIKLG 95
                                        EKNSNOLLSOGDEITVG
                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                         ORFNames=DEHA0G22440g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 430:35-44(2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=284592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CBS767;
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29
                                   13 GRSSSCDVRI-NGNDVSSKHCKLTLTINNNREYLCIKDLSSNGTYLNDEIIGKDSSILLR 71
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4 GRNPACDYHLGNISRLSNKHFQILXX - - - - XXXXLLNDISTNGTWLNGQKVEKNSNQLLS
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PubMed=14656965; DOI=10.1101/gr.1295503;
Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.,
"Comparative genome analysis of Vibrio vulnificus, a marine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
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Choy H.E.;
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Vibrionaceae; Vibrio.
NCBI_TaxID=196600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016809; AA007399.1; -.
InterPro; IPR000253; FHA.
InterPro; IPR00884; SMAD_FHA.
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SEQUENCE 374 AA, 42554 MW; F42608D67A766FE9 CRC64;
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FHA DOMAIN; 1.

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PS50006;
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A Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
A Elking T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
A Elking T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
A cui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
A Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte B., Greenberg D.,
A Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
A Roy A., Ramussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
A Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
A Cogoni C., Macino G., Catcheside D., Li W., Pertt R.J., Osmani S.A.,
A Pesouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
A Yarden O., Plamann M., Seiler S., Dunlap J., Rafford A., Aramayo R.,
A Natvig D.O., Alex L.A., Mannhaupt G., Ebizen B.,
A Natvig D.O., Alex M.S., Lander E.S., Nusbaum C., Birren B.,
A Markel Sequence of the Filamentous Fungus Neurospora crassa.;
                                                                                                                                                                                                                                                                                                                                                                                               FGRSESCDWVLPDPPERIISGVHGEITKFGNDYLLRDLSTNGIFVNKSVSPVGNGVEVALN 122
                                                                                                                                                                                                                                                                                                                                                                 3 FGRNPACDYHLGNISR-LSNKHFQILXXXXXXLLNDISTNGTWL-----NGQKVEKN 53
                                                                                                                                                                                                                                                                                                               10; Gaps
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GO:0004674; F.protein serine/threonine kinase activity; IEA.
GO:0016740; F.transferase activity; IEA.
GO:0006468; P.protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                          th 27.1%; Score 91; DB 2; Length 434; Similarity 35.1%; Pred. No. 0.0039; 26; Conservative 13; Mismatches 25; Indels
                                                                                                                                                                                                       434 AA; 49606 MW; E5E36BA5E1A7CCC0 CRC64;
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Last sequence update)
Last annotation update)
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GO; GO:0004674; F:protein serine/threon
GO; GO:0016740; F:protein serine/threon
GO; GO:0016740; F:transferase activity;
GO; GO:0006468; P:protein amino acid ph
InterPro; IPR001009; Kinase like.
InterPro; IPR0010109; Kinase like.
InterPro; IPR008271; Ser thr psin AS.
InterPro; IPR008271; Ser thr psin AS.
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                     Genome Res. 13:2577-2587(2003).
EMBL; AP005348; BAC97021.1; -.
InterPro; IPR000253; FHA.
InterPro; IPR08984; SMAD_FHA.
PEam; PF00498; FHA; 1.
PROSITE; PS50006; FHA_DOMAIN; 1.
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Pfam; PF00069; Pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
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123 DKDVINFGDYEIEV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 SNQLLSQGD-EITV 66
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HSSP; P49137; 1NXK.
                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                  Complete proteome. SEQUENCE 434 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0:0-0(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                    63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q7SEKO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q7SEK0
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Q7SEK0
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GO; GO:0004574; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016468; P:protein amino acid phosphorylation; IEA.
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Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AB118105; BAC82422.1; -.
                                                                                                                                                                                                                 Query Match 26.6%; Score 89.5; DB 2; Length 712; Best Local Similarity 32.9%; Pred. No. 0.011; Matches 23; Conservative 14; Mismatches 28; Indels
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PROSITE; PSSOOLO7; FRA DOMAIN; 1.
PROSITE; PSSOOLO7; PROTEIN KINASE ATP; 1.
PROSITE; PSSOOLO1; PROTEIN KINASE DOM; 1.
PROSITE; PSOOLO8; PROTEIN KINASE DOM; 1.
ATP-binding; Hypothetical protein; Kinase;
Serine/threonine-protein kinase; Transferase.
GerimeNCR 398 AA; 45596 MW; E9C6ADID96A49CB5 CRC64;
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE SY; 1.
ATP-binding; Hypothetical protein; Kinase;
Serine/threonine-protein kinase; Transferase.
SEQUENCE 712 AA; 79186 MW; ASEA2536542B339B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Entamoeba histolytica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 26.5%; Score 89; DB 2;
Best Local Similarity 42.1%; Pred. No. 0.0066;
Matches 24; Conservative 8; Mismatches 21
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InterPro; IPR01009; Kinase like.
InterPro; IPR0101009; Kinase like.
InterPro; IPR000219; Ser thr pkinase.
InterPro; IPR008271; Ser thr pkinase.
InterPro; IPR008271; Ser thr pkinase.
InterPro; IPR001245; Tyr pkinase.
Pfam; PP00069; Pkinase; I.
ProDom; PD000001; Prot_kinase; I.
SMART; SM00210; STRC; I.
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258 ELQELDEIAV 267
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SMART; SM00240; FHA; 1.
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Q10292;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome analysis of Photobacterium profundum reveals the complexity of
                                                                                                                                                                                                                                                                                                                                                                                                                                   Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
Cegtaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21359325; Dibmed=11466286; Disminstrate Control of STRAIN=ATCC 824 Dismed=11466286; Doi=10.1128/JB.183.16.4823-4838.2001; Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Noelling J., Breton G., Omelchenko M.V., Mitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P., Gaisson R.J., Bennett G.N., Koonin E.V., Smith D.R.; "Genome sequence and comparative analysis of the solvent-producing J. Bacterium Clostridium acetobutylicum."; J. Bacteriol. 183:4823-4838(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium acetobutylicum.
Bacteria, Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.0%; Score 87.5; DB 2; Length 436; 36.8%; Pred. No. 0.011; Live 11; Mismatches 27; Indels E
                                                                                                                                                                                                                                                   Photobacterium profundum (Photobacterium sp. (strain SS9)). Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceas; Photobacterium. VCBI_TaxID=74109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       high pressure adaptations.";
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR378665; CAG19079.1; -.
InterPro; IPR000253; FHA.
InterPro; IRR008984; SWAD_FHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome. -- SEQUENCE 436 AA; 49951 MW; 29ECBDD8C5CEBAC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-07T-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
OrderedLocusNames=PBPRA0658;
                                      436 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 AA
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OrderedLocusNames=CAC0504;
                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50006; FHA_DOMAIN; 1.
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InterPro; IPR008984; SMAD_FHA.
Pfam; PF00498; FHA; 1.
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HSSP; P46013; 1R21.
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NCBI_TaxID=1488;
                                                                                            05-JUL-2004
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RA Squares J. Peat N., Rajandream M.A., Lyne M., Lyne R., Stewart A., Rodod V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Ragouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., RA Brown D., Brown S., Chillingworth T., Churcher C.M., A Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., RA Gentles S., Goble A., Hamlin N., Harris D., Hidayo J., Hodgen G., RA Holroyd S., Hornsby T., Howarth S., Huchle E.J., Hunt S., Jagels K., Holroyd S., Hornsby T., Howarth S., Huchle E.J., Hunt S., Jagels K., A James K., Jones L., Jones M., Leather S., McDonald S., McLean J., RA James K., O'Neil S., Randers R., Studers S., Stevens K., Cliver K., O'Neil S., Randers R., Squares S., Stevens K., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Raylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Rodour J., Volckaert G., Aert R., Robben J., Gyrmonprez B., Meltjens I., Bock A., Lehrach H., Reinhardt R., Pohl T.M., RA Goffeau A., Cadieu E., Derano S., Gloux S., Lelaure V., Mottier S., Rager P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Ause S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., A Centti L., Lowe T., Moreno S., Armstrong J., Forsburg S.L., A Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Potashkin J., The Genome sequence of Schizosaccharomyces pombe.";

R. Nature 415:811-88012002.
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                                                                                                                                                                                                                                                                                          2 TFGRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQ
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-ULL-2004 (Rel. 44, Last annotation update)
Meiosis-specific serine/threonine-protein kinase mek1 (EC 2.7.1.37).
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--- CATALTIC ACTUITY: ATP + a protein = ADP + a phosphoprotein.
--- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
--- SIMILARITY: Contains 1 FHA domain.
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                                                                                                                                                   Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
                                                                                                                                                                                                                   29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lyne M.H., Bryant J.A., Aves S.J.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
PROSITE; PS50006; FHA_DOMAIN; 1.
Complete protecome.
SEQUENCE 159 AA; 17667 MW; F4F44A3D3BF05AA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                               25.9%; Score 87; DB 2; 37.3%; Pred. No. 0.0044;
                                                                                                                                                                                                                      9; Mismatches
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Schizosaccharomyces pombe (Fission yeast)
                                                                                                                        Query Match
Best Local Similarity 37.3*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 GDEİKIĞ 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces.
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opportunistic pathogen.";
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 271478; CAAS6101.1; -

DR EMBL; 298596; CAB1196.1; -

DR EMBL; 298596; CAB1196.1; -

DR EMBL; 298596; CAB1196.1; -

DR EMBL; 298596; CAB1196.1; -

DR HIS.P. 74420; TA3420.

BR GeneDB SPombe; SPACT4C4.03; -

DR InterPro; IPR000213; FHA.

DR InterPro; IPR000219; Prot thin sellike.

DR InterPro; IPR00821; Ser_thr_pkin_AS.

DR InterPro; IPR00821; Ser_thr_pkin_AS.

DR InterPro; IPR00891; Ser_thr_pkin_AS.

DR InterPro; IPR00891; Ser_thr_pkin_AS.

DR InterPro; IPR00891; FHA, 1.

DR Ffam; PP00009; FHA, 1.

DR Ffam; PP00009; FHA, 1.

DR FROMITE; PS000001; Prot kinase; 1.

DR SWART; SW00220; STKC; 1.

DR PROSITE; PS00101; PROTEIN KINASE DOM; 1.

DR PROSITE; PS00101; PROTEIN KINASE DOM; 1.

DR PROSITE; PS00101; PROTEIN KINASE ST; 1.

DR ATP-binding; Melosis; Serine/threonine-protein kinase; Transferase.

T DOMAIN 166 421 Protein kinase.

T DOMAIN 166 421 Protein kinase.

T NE SITE 281 281 281 Protein acceptor (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE_20437337; PubMed=10984043; DOI=10.1038/35023079; Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoquchi S.D., Warrener P., Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoquchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Madman S., Yuan Y., Brody L.L., Coulter S.M., Polger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Protein kinase.

ATP (By similarity).

Proton acceptor (By similarity)

FOR By similarity).

6D62D79E9A1B45E0 CRC64;
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Last annotation update)
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160 421 Prc
166 174 ATI
281 Prc
189 189 ATI
445 AA; 51151 MW; 6
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OrderedLocusNames=PA0081;
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BINDING
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Ack Pubbed-14702039; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/ng1285; DOI-10.018/
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Q96EPI; Q96SL3; Q9NRT4; Q9NT32; Q9NVD5;
29-MAR-2004 (Rel. 43, Last sequence update)
25-GCT-2004 (Rel. 45, Last annotation update)
Ubiquitin ligase protein CHFR (EC 6.3.2.-) (Checkpoint with forkhead and RNNG finger domains protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scolnick D.M., Halazonetis T.D.; "Chfr defines a mitotic stress checkpoint that delays entry into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tch 25.4%; Score 85.5; DB 2; Length 497; al Similarity 33.3%; Pred. No. 0.024; 23; Conservative 13; Mismatches 30; Indels 3
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Nature 406;959-964(2000).

BMBL; AE004447; AE003471.1; -.

PIR; P83634; P83634.

InterPro; IPR000253; FHA.

InterPro; IPR008984; SMAD_FHA.

FMAM; PF00498; FHA; 1.

SMART; SM02240; FHA; 1.

PROSITE, PSS0006; FHA; 1.

COMplete proteome; Hypothetical protein.

SEQUENCE 497 AA; 53310 MW; A6C63EID287E7272 CRC64;
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89 QDGETVRLG 97
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Best Local Similarity
Matches 23; Conserv
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Tataubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION, AUTOUBIQUITINATION, AND MUTAGENESIS OF ILE-306 AND TRP-332. PubMed=11807099; DOI=10.1083/jcb.200108016; Kang D., Chen J., Wong J., Fang G.; "The checkpoint protein Offr is a ligase that ubiquitinates Plk1 and inhibits cdc2 at the G2 to M transition.";
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inhibitors in gastric cancer.";
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"CHFR-associated early G2/M checkpoint defects in breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISEASE, AND VARIANTS NSCLC LEU-166; PRO-202 AND SER-536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION, AND MUTAGENESIS OF THR-39 AND SER-205
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                                                                                                                tumors.";
                                                                                                             "Epigenetic inactivation of CHFR in human tumors. Proc. Natl. Acad. Sci. U.S.A. 100:7818-7823 (2003)
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PATHWAY: Ubiquitin conjugation; third step.
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IsoId=Q96EP1-2; Sequence=VSP_009349;
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-i- SUBCELLULAR LOCATION: Nuclear.
-i- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human lung cancer.";
Cancer Res. 63:7185-7189(2003).
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strain 1.";
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CHFR_MOUSE
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                                                                                                                                                                                                                                                                                                     1 WIFGRNPACDYHLGNISRLSNKHFQIL--XXXXXXLLNDISTNGTWLNGQKVEKNSNQLL
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
PubMed=14752164; DOI=10.1126/science.1093027;
Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
Sockett R.E., Schuster S.C.;
"A predator unmasked: 1ife cycle of Bdellovibrio bacteriovorus from egenomic perspective.";
"A predator unmasked: 1ife cycle of Bdellovibrio bacteriovorus from Science 303:689-692(2004).
EMBL; BX842647; CAE78455.1; -.
               Note=No experimental confirmation available;
TISSUE SPECIFICITY: Ubiquitous.
DEVELOPMENTAL STAGE: Weakly expressed in Gl phase, and highly expressed during 8 phase.
DOMAIN: The FHA domain may be required to interact with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bdellovibrio bacteriovorus,
Bacteria, Proteobacteria, Deltaproteobacteria, Bdellovibrionales,
Bdellovibrionaceae, Bdellovibrio.
                                                                                                                                                                                                                                   .;
7
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                                                                                                                                                                                         25.3%; Score 85; DB 1; Length 664; 34.8%; Pred. No. 0.038; tive 6; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     674 AA; 75694 MW; E898524FE1A87766 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 27, Last sequence update) (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  674 AA.
Isold=Q96EP1-3; Sequence=VSP 009350;
                                                                                                                           phosphorylated proteins. -- PTM: Autoubiquitinated in vitro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7UIF2 PRELIMINARY; PRT; Q7UIF2; 01-OCT-2003 (TrEMBLrel. 25, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50006; FHA DOMAIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000253; FHA.
InterPro; IPR008994; SMAD FHA.
InterPro; IPR008991; TPR-Tike.
Pfam; PP00498; FHA; 1.
SMART; SM00240; FHA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OrderedLocusNames=Bd0474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 29.9
                                                                                                                                                                                                          Similarity 34.8
23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                59 SQGDEI 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=959;
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05-JUL-2004
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                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 30
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ID Q7
AC Q7
DT 01
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4 GRNPACDYHL--GNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQ 60
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Q810G13, Q8BAT29; Q8BMT4;
29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annocation update)
ubiquitinn ligase protein CHFR (EC 6.3.2.-) (Checkpoint with forkhead and RING finger domains protein).
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MEDLINE-22354683; PubMed=1246685; DOI=10.1038/nature01266;
Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
Blake J.A., Bradat D., Brusic V., Chothia C., Corbani L.E., Cousins S
Dalla E., Dragani T.A., Fletcher C.F., Fortest A., Frazar K.S.,
Gaasterland T., Gariboldi M., Gissi C., Godaik A., Gough J.,
Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100; Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R.; "Complete genome sequence of the marine planctomycete Pirellula sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                     Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales; Planctomycetaceae; Pirellula.
NCBL_TaxID=117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 25.0%; Score 84; DB 2; Length 346
Best Local Similarity 32.8%; Pred. No. 0.025;
Matches 22; Conservative 16; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 AA; 38128 MW; D22946CE39B91677 CRC64;
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
EMBL; BX294155; CAD77662.1; -.
HSSP; P46014; 1MZK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000253; FHA.
InterPro; IPR000253; FHA.
InterPro; IPR000160; GGDEF.
InterPro; IPR008984; SMaD_FHA.
Pfam; PF00498; FHA; 1.
Pfam; PF00590; GGDEF; 1.
SMART; SM00267; DUPI; 1.
SMART; SM00240; FHA; 1.
TIGRFAM8; TIGR00254; GGDEF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50006; FHA DOMAIN; 1.
PROSITE; PS50887; GGDEF; 1.
                                                                                                                   OrderedLocusNames=RB12571;
                                                                                                                                                      Rhodopirellula baltica
                                                                                 GGDEF family protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                || : :|
155 GDTVRIG 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome. SEQUENCE 346 AA;
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

Santana R., Takenaka Y., Taylor M.S., Teaddale R.D., Tomita M.,

Norardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

Wilming L.G., Wynnaw-Boris A., Yangisawa M., Yang I.,

Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Pukuda S.,

Aliraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Pukuda S.,

Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

Wasanishih A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

Birney B., Hayashizaki Y.;

Malyasaki A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

Birney B., Hayashizaki Y.;

Malyasaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

Ranishih A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

Malyasaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

Malyasaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

Malyasaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

Malyasaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

Malyasaki A., Washino M., Waterston R., Lander B.S., Rogers J.,

Malyasaki A., Malyashizaki Y.;

Malyasaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

Malyasaki A., Washino M., Waterston R., Lander B., Shibata K., Shinagawa A.,

Malyasaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

Malyasaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

Malyasaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

Malyasaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

Malyasaki A., Sakai K., Sasaki D., Shibata K., Shinagawa I.,

Malyasaki A., Sakai K.,
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Altschul S.F., Zeeberg B.B., Boraldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunstane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Raher J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalak B., Smilus D.E.,
B. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note=No experimental Confirmation available,
Note=No experimental Confirmation available,
DOWAIN: The FHA domain may be required to interact with
phosphorylated proteins (By similarity).
PTM: Autcoubiquitinated in vitro (By similarity).
PTM: Phosphorylated by PKB. Phosphorylation may affect its E3
ligase activity (By similarity).
SIMILARITY: Contains 1 FHA domain.
SIMILARITY: Contains 1 FHA domain.
CAUTION: According to some authors it can ubiquitinate and promote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

-!- FUNCTION: E3 ubiquitin-protein ligase required to transfently arrest cells in early prophase when they are exposed to microtubule poisons. Acts in early prophase before chromosome condense, when the centrosome move apart from each other along the periphery of the nucleus. Probably promotes the formation of Lysebalphery of the nucleus. Probably promotes the formation of Lysebalphery of the nucleus. Probably promotes the formation of Lysebalinked polyubiquitin chains and functions with the specific ubiquitin-conjugating UBC13-MMS2 (UBE2N-UBE2N2) heterodimer.

Substates that are polyubiquitinated at Lys-63 are usually not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      targeted for degradation, but are rather involved in signaling cellular stress. This suggests that it may be involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 signaling the presence of mitotic stress caused by microtubule poisons (By similarity).
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SUBCELLULAR LOCATION: Nuclear (By similarity).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q810L3-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 WIFGRNPACDYHLGNISRLSNKHFQIL--XXXXXXLLNDISTNGTWLNGOKVEKNSNQLL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 WIIGRRRGCDLSFPSNKLVSGDHCKLTVDEISGEVTLEDTSTNGTVINKLQVVKKQTYPL 97
              involved in mitotic progression. However, as experiments have been done either in vitro or with extracts from Xenopus, there is actually few evidence for a role of CHFR in protein degradation in vivo.
                                                                                                                                                                                                                                                                                                                                   STRAIN=Biotype gravis / NCTC 13129;
MEDLINE=22965443; PubMed=14602910; DOI=10.1093/nar/gkg874;
Medeno-Tarraga A.-M., Efstratiou A., Dover L.G., Holden M.T.G.,
Pallen M.J., Bentley S.D., Besra G.S., Churcher C.M., James K.D.,
De Zoysa A., Chillingworth T., Cronin A., Dowd L., Feltwell T.,
degradation of substrates such as PLK, a protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.0%; Score 84; DB 1; Length 664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Missing (in isoform 2).
/FIId=VSP_009351.
C - H (in Ref. 1).
G - C (in Ref. 1).
W; D651BE3E463DEBB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterineae; Corynebacteriaceae; Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative signal transduction protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.051;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 AA.
                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                          MGD; MGI:2444898; 5730484M20Rik.
                                                                                                                                                                                                               EMBL; AK052473; BAC35008.1; -. EMBL; AK077629; BAC36912.1; -. EMBL; BC049792; AA449792.1; -. HSSP; Q96EP1; 1LGP.
                                                                                                                                                                                                                                                                                        InterPro; IPR000253; FHA.
InterPro; IPR008984; SMAD_FHA.
InterPro; IPR001841; Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73871 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 33.3
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        664 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 SQGDEI 64
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VARSPLIC
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CONFLICT
SEQUENCE
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Q6NHD4
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272 VITVG 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=959;
                                                                                                                                                                                                                                                                                                                                                   efficiens.";
                                                                                                                                                                                                                                                                                                           Gojobori T.;
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                                                                  QBFUH9
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Matches
                                        RESULT 35
Q8FUH9
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                                                                                                                                                                                                                                                                 2 TFGRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Biocype gravis / NCTC 13129;
MEDLINE=2265543; PubMed=14602910; DOJ=10.1093/nar/gkg874;
Cerdeno-Tarraga A.-M., Efstratiou A., Dover L.G., Holden M.T.G.,
Pallen M.J., Bentley S.D., Besra G.S., Churcher C.M., James K.D.,
De Zoysa A., Chillingworth T., Cronin A., Dowd L., Feltwell T.,
Hamlin N., Holroyd S., Jagels K., Moule S., Quail M.A.,
Rabbinowitsch E., Rutherford K.M., Thomson N.R., Unwin L.,
Whitehead S., Barrell B.G., Parkhill J.;
"The complete genome sequence and analysis of Corynebacterium
           Rabbinowitsch E., Rutherford K.M., Thomson N.R., Unwin L., Whitehead S., Barrell B.G., Parkhill J.;
Whitehead S., Barrell B.G., Parkhill J.;
The complete genome sequence and analysis of Corynebacterium diphtheriae NCTC11129.";
Nucleic Acids Res. 31:6516-6523(2003).
EMBL; BX248157; CAR49731.1;
InterPro; IPR000253; FHA.
InterPro; IPR00049; FHA.
Fran, PP004998; FHA; 1.
SMART; SM00240; FHA; 1.
SMART; SM00240; FHA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.9%; Score 83.5; DB 2; Length 288; 38.5%; Pred. No. 0.024; ive 10; Mismatches 25; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacceria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacterium.
                                                                                                                                                                                                        Match 24.9%; Score 83.5; DB 2; Length 143; Local Similarity 31.3%; Pred. No. 0.011; es 21; Conservative 17; Mismatches 24; Indels
Hamlin N., Holroyd S., Jagels K., Moule S., Quail M.A.,
Rabbinowitsch E., Rutherford K.M., Thomson N.R., Unwin L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50006; FHA DOMAIN; 1.
Complete protecome; Hypothetical protein.
SEQUENCE 288 AA; 31558 MW; AB8B52C505D89241 CRC64;
                                                                                                                                                                              143 AA; 15264 MW; 7BE05BBB76F8DB1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                       288 AA
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Nucleic Acids Res. 31:6516-6523(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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InterPro, IPR008984; SMAD_FHA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OrderedLocusNames=DIP0059;
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nes 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                 proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1717;
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                                                                                                                                                                 Complete
                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                   QENKG7;
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227 GRSNDADLRLPD-TGVSRQHAEITWDGRDAILVDLKSTNGTTVNDTPVE---NWLLADGD 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
PubMed=14752164; DOI=10.1126/science.1093027;
Rendulic S., Jagtap P., Roshuns A., Eppinger M., Baar C., Lanz C., Sockett R.I., Lambert C., Evans K.J., Goesmann A., Meyer F., Sockett R.E., Schuster S.C.;
"A predator unmasked: life cycle of Bdellovibrio bacteriovorus from genomic perspective.";
Science 303:689-692(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bdellovibrio bacteriovorus.
Bacteria, Proteobacteria, Deltaproteobacteria, Bdellovibrionales,
Bdellovibrionaceae, Bdellovibrio.
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                                                                                                                                                                                                                                                                                                                        STRAIN=YS-314;
MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
Mishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E., Sugimoto S., Matsul K., Yamagishi A., Kikuchi H., Ikeo K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 24.9%; Score 83.5; DB 2; Length 298; Local Similarity 40.0%; Pred. No. 0.025; tes 26; Conservative 10; Mismatches 24; Indels
                                                                                                                                                                                               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Res. 13:1572-1579(2003).

EMBL; AP002214; BAC16849.1; -.

HSSP; 946014; IMZK.

InterPro; IPR000253; FHA.

InterPro; IPR008984; SMAD_FHA.

Pfam; PF00498; FHA; 1.

SMART; SM00240; FHA; 1.

PROSTTE; PSC0006; FHA, 10.

Complete proteome; Hypothetical protein.

SEQUENCE 298 AA; 32166 MW; ACAD78F03746781F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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Last annotation update)
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298 AA.
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05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
Hypothetical protein.
OrderedLocusNames=Bd0472;
                                               Created)
PRT;
                                                                      01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25, Hypothetical protein.
                                               01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                             OrderedLocusNames=CE0039;
                                                                                                                                                                          Corynebacterium efficiens
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PRELIMINARY;
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4 GRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQGD 62
                                                                                                                                                                                                                                                                      "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; AP005274; BAB97440.1; -.
INESPP; P46014; IMZK.
InterPro; IPR000253; FHA.
InterPro; IPR000253; FHA.
SMART; SM00240; FHA; 1.
SMART; SM00240; FHA; 1.
SMART; P650066; FHA DOMAIN; 1.
COMPLETE POSCOOG; FHA DOMAIN; 1.
SCOUPLEE 288 AA; 31317 MM; 1E0E67A6F95AA791 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kalinowski J., Bathe B., Bartels D., Bischoff N., Bott M., Burkovski A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat L., Goesmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B., McHardy A.C., Meyer F., Moockel B., Pfefferle W., Puehler A., Rey D.A., Rueckert C., Rupp O., Sahm H., Wendisch V.F., Wiegraebe I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins.";

July Atamins.";

BABL; BX927148; CAF18615.1;

InterPro; IPR000253; FHA.

InterPro; IPR00094; SMAD_FHA.

FFam; PF00498; FHA; 1.

SMART; SM0240; FHA; 1.

PROSITE; PS50006; FHA DOMAIN; 1.

PROSITE; PS50006; FHA DOMAIN; 1.

SEQUENCE 298 AA; 32347 MW; OBF6ASOBA2448EF2 CRC64;
                                                                                                            Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
24.3%; Score 81.5; DB 2; Length 288;
Best Local Similarity 38.5%; Pred. No. 0.044;
Matches 25; Conservative 11; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025 Nakagawa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
PubMed=12948626; DOI=10.1016/S0168-1656(03)00154-8;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein Cg10047.
CorderedLocusNames=Cg10047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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OrderedLocusNames=cg0064;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273 VITVG 277
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                                                                                                                                                                                 NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1718;
                                                                                                                                                                                                                                                               Nakagawa S.;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                        2 TFGRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQ 60
                                                                                                                                                                                                                                                                                4 GRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGQKVEKNSNQLLSQGD
                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium
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Nishito Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E.,
Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
Gojobori T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.3%; Score 81.5; DB 2; Length 142; 32.8%; Pred. No. 0.021; ive 15; Mismatches 25; Indels 5
                                                                                                                                                                                               Query Match 24.6%; Score 82.5; DB 2; Length 557; Best Local Similarity 34.4%; Pred. No. 0.067; Matches 22; Conservative 15; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OrderedLocusNames=CE1573;
Corynabacterium efficiens.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Res. 13:1572-1579(2003).

EMBL; AP005219; BAC18383.1; -.
HSSP; P46014; IMZK.

HIGEPPC; IPR000253; FHA.
ILLEPPC; IPR008984; SMAD_FHA.

Edm; PF00498; FHA; 1.

PROMITE; PS50006; FHA_DOMAIN; 1.

COMPLE PS50006; FHA_DOMAIN; 1.

COMPLE PS50006; FHA_DOMAIN; 1.

SROUENCE 142 AA; 15096 MW; 97C64454E33A1238 CRC64;
                                  InterPro; IPR000253; FHA.
InterPro; IPR000984; SMAD_FHA.
Pfam; PF00498; FHA; 1.
SMART; SM00240; FHA; 1.
PROSITE; PS50006; FHA_DOMAIN; 1.
Complete proteome.
SEQUENCE 557 AA; 60066 MW; C057EB85BF578A20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
              EMBL; BX842647; CAE78453.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 23, (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                           :: :
KLGI 85
                                                                                                                                                                                                                                                                                                                                                                  EITV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=YS-314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               efficiens.";
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Q8NU92;
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RESULT 37

쉽 ઠે 셤 Matches

셤 ð RESULT 38

08NU92 ID 08 AC 08

Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                               4 GRNPACDYHLGNISRLSNKHFQILXXXXXXLLNDI-STNGTWLNGOKVEKNSNQLLSQGD
                                  5; Gaps
                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Query Match

24.3%; Score 81.5; DB 2; Length 298;
Best Local Similarity 38.5%; Pred. No. 0.046;
Matches 25; Conservative 11; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Bristol N2;
MEDLINE=9965613; PubMed=9851916;
The C. elegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for investigating biology.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 24.1%; Score 81; DB 1; Length 952; Local Similarity 41.2%; Pred. No. 0.19; es 14; Conservative 9; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 100 FHA.
952 AA; 105274 MW; D9CFB0AB3C685FBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 LLNDISTNGTWLNGOKVEKNSNQLLSQGDEITVG 67
                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Hypothetical protein COIGG.5 in chromosome III
ORFNames=COIGG.5;
                                                                                                                                                                                                                                                    952 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 282:2012-2018(1998).
-!- SIMILARITY: Contains 1 FHA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MormBase; Libea; i, i, i, i, i, i, wormBase; WBGene00007227; C01G6.5. WormPep; C01G6.5; CE00867. InterPro; IPR000253; FHA. InterPro; IPR008984; SMAD_FHA. FEam; PF00498; FHA; 1. SMART; SM00240; FHA; 1. PR0STE; PS00066; FHA_DOMAIN; 1.
                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z35595; CAA84636.1; -. PIR; T18837; T18837.
                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
                                                                                                                                                                 283 VITVG 287
                                                                                                                                  63 EITVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
                                                                                                                                                                                                                                                    CAEEL
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Search completed: February 24, 2005, 15:23:38 Job time : 128.285 secs

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